Listing for I hears \* . 31

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Page

(MT)

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 19 09:53:17 1996; MasPar time 7.39 Seconds 555.014 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: 4162 1 MESSKKMDSPGALQTNPPLK.....IKDDT1F1KVIVDTSDLPDP 567 >US-08-404-832-2 (1-567) from US08404832.pep

Searched: PAM 150 Gap 11 62355 seqs, 7230759 residues

Scoring table:

3 •

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq20
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12

Statistics: Mean 36.298; Variance 168.378; scale 0.216

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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987654321	Result
132 132 128 128 130 130 145 118 116	Score
2222222222	Query Match
527 527 235 320 885 1284 252 334 337	Query Match Length DB
7 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	BB
R38099 R14183 P94260 P94366 R66930 P81187 P94369 R51227 R63681	IĐ
Schistosomula mansoni 8.41e-02 Product of clone IrV- 8.41e-02 41kD protein of T. co 1.63e-01 41kD protein of T. co 1.63e-01 AMMI chromosome inv(1 1.17e-01 Sequence encoded by a 2.66e-01 Fusion protein congt. 8.27e-01 Membrane antigen pept 1.14e-00 Merosin amino acids 1 9.71e-01	Description
8.41e-02 8.41e-02 1.63e-01 1.63e-01 1.17e-01 2.66e-01 8.27e-01 1.14e+00 9.71e-01	Pred. No



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111 111 112 112 112 112 112	, , , , , , , , , , , , , , , , ,
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Truncated PVX replica Truncated PVX replica PVX replicase. Human nestin protein Human nestin protein Human apoAIV mutein P P. falciparum LSA-R-NH PUMAN apoAIV mutein P Human ap	Hyaluronan receptor.  Hyaluronan receptor.  Portion of peptide an Yeast topoisomerase I p100 protein from hum Ro/SSA autoantigen.  AMMI chromosome inv(1 Human Duchenne muscul Fragment of 101 kD proficinarim ISA Nate
	9.71e-01 8.27e-01 1.57e+00 2.52e+00 2.52e+00 4.70e+00 2.94e+00 4.02e+00 8.71e+00 8.71e+00

#### ALIGNMENTS

T 1 R38099 standard; Protein; 527 A R38099; 26-OCT-1993 (first entry) 26-OCT-1993 (first entry) Schistosomula mansoni epitope; glyc schistosomula; myosin; C. elegg schistosoma mansoni. US5219566-A. 15-JUN-1993. 30-SEP-1988; US-252075. 30-SEP-1988; US-252075. 09-JUL-1991; US-275804. (UYJO) UNIV JOHNS HOPKINS. STrand M; WPI; 93-205255/25. WPI; 93-205255/25.	T 1 R38099; R38099; R38099; 26-CCT-1993 (first entry) Schistosomula mansoni epitope. Schistosomula; myosin; C. elegans. Schistosomula; myosin; C. elegans. Schistosoma mansoni. US5219566-A. 15-UUN-1993. 30-SEP-1988; US-252075. 30-SEP-1988; US-252075. 09-UUL-1991; US-725804. (UYJO) UNIV JOHNS HOPKINS. Strand M; WPI; 93-205255/25. N-PSDB; 043521.	
	A.  anic epitope; ns.	T 1 26-0CT-1993 (first entry) 26-0CT-1993 (first entry) Schiistosomula mansoni epitope. Antibody; protein epitope; glycanic epitope; surface; schiistosomula; myosin; C. elegans. Schistosoma mansoni. US521956-A. US521956-A. 15-JUN-1993. 30-SEP-1988; US-252075. 30-SEP-1988; US-252075. 30-SEP-1988; US-252075. 30-SEP-1988; US-252075. Strand M; Strand M; WF1; 93-20525/25. N-PSDB; Q43521. N-PSDB; Q43521. New cDNA encoding polypeptide of Schistosoma mansoni - includes



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RESULT RE
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The polypeptide binds to antibodies which recognise protein epitopes, but not glycanic epitopes, expressed on the surface of live schistosomula of S. mansoni. The protein epitopes are common to a 200 kD and a 38 kD glycoprotein of S. mansoni. These glycoproteins are immunologically cross-reactive with myosin heavy chains from other species. However, anti-myosin antibodies directed against myosin mols. of other species are not cross-reactive with the surface epitopes of
                             lambda-gtl1 with anti-IrV sera raised against a subset of adult antiqens. The sequence is thought to at least partially encode schistosome myosin. It has 48% identity with the myosin heavy chain of C. elegans. The DNA can be used to produce a fusion pr with beta galactosidase sequences. The product can be used as a immunogen to produce vaccines against bilharziasis.
                                                                                                                                                                                                                      Polypeptide(s) specific for epitope(s) of Schistosoma mansoni used as vaccines against bilharziasis.
Claim 5; Fig 1B; 10pp; English.
The clone was obtd. by screening an adult worm cDNA library in
                                                                                                                                                                                                                                                                                                                                                                                      WPI;
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03-JAN-1992
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R14183 standard; Protein;
   with beta galactosidase sequences. The immunogen to produce vaccines against Sequence 527 AA;
                                                                                                                                                                                                                                                                                                                                                     N-PSDB; Q13982.
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30-SEP-1988;
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Modified -site 218
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larity 24.4%;
Conservative
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US-252075.
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Pred. No. 8.41e-02;
33; Mismatches 51;
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Score

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Length

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RESULT
ID P
AC P
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DE 4
DE 4
EW P.
OS T.
PN W.
PD 1.

13-UN-1990 (first entry)
41kD protein of T. colubriformis.
Parasitic nematode; 41 kD protein.
Trichostrongylus colubriformis.

12-JAN-1989. 06-JUL-1988; AU0239 Trichostrongylus W08900163-A. Ş

299

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356

67 leekekkvqeaeaevaalnrrmtlleeeleraeerlkiateklee

IEIERQKEMLRNN--ESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEA-DSMKSSVES

355

LQNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLAD

LT 4 P94366

standard;

protein;

320

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P94366;

-6 7.8

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Page

4

HESULT HESULT PAR AC PRINCE PAR AC PRINCE PAR AC CC PRINCE PAR AC CC CC PRINCE PAR AC δõ В S В 밁 Matches Query Match Best Local Best Matches N-PSDB; N91210.
Protein derived from parasitic nematode species - uprotective immunity against nematode parasites of m Disclosure; ; 57pp; English.
Recombinant organisms contg. DNA encoding the prote produce polypeptide which is capable of protecting against parasitism from T. colubriformis.
See also P94366-P94369. P94260 P94260; Wagland WPI; 89-06-JUI\_1988; AU0239. 07-JUI\_1987; AU-002940. (BICT-) Biotechn Austr Pt, (CSIR) Commonwealth Cobon GS, Austen RA, O'Donnell IJ, Frenkel MJ, 41kD protein of T. colubriformis. Parasitic nematode; 41kD protein. Sequence WO8900163-A. Trichostrongylus colubriformis. 315 demeenlareqkirgdvekskrkleg-dlkatq-etvd-dlervkrd---leeqlrrke 3-JUN-1990 255 dneirtlqsemagqdemigklnkdkknleeenkrtqealqaeedkvnhlnklkaklestl 330 KELDKEIRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQVARNTGLLESQLSRHD 270 EKKVSLIQNESVEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKL 329 Local 7 mkiekdnaldradaaeekvrqiteklerveeelrdtqkkmmqtendldkaqedlaaatsq 89-039628/05. standard; n 3.1%; Similarity 17.1%; 18; BM Similarity 29; Conse 235 AA; Conservative arity 24.4%; Conservative (first protein; entry) 235 Score Pred. 35; M Pred. A Mismatches Mismatches 128; DB 1; No. 1.63e-01; No. 8.41e-02; atches 51; 49; protein can be used Sci and Kennedy Length 235 man a Indels Indels guinea d to Ind Res Orgn. WPK, Savin KW, provide animal.s pigs μ 6 Gaps Gaps 388 367 66 to 314 4; 2

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Page S

RESULT
RE S В á В Query Match Best Local Matches N-PSDB; 084589.

N-PSDB; 084589.

Novel DNA spanning the pericentric inversion of chromosome 16 for the screening of acute myeloid leukaemia
Claim 4; Page 34-38; 78pp; English.

PCR was performed on total cellular RNA from 5 AMMI patients having
a pericentric inversion of chromosome-16, M4Eo subtype. Sequencing
showed the inv(16) fusion to comprise a sequence from the CBFB
gene, encoding a novel transcription factor, and the MYH11 gene,
encoding smooth muscle myosin heavy chain. In 1 patient, nt 1-492
of the CBFB gene were fused to nt 994 of MYH11 (shown in Peptide /label= MYH11 WO9504067-A. protective immunity against nematode parasites of man and Claim 4; page 39; 57pp; English. Recombinant organisms contg. DNA encoding the protein can produce polypeptide which is capable of protecting guinea against parasitism from T. colubriformis. See also P94260, and P94368-P94369. N-PSDB; N91211.

Protein derived from parasitic nematode species - used 26-JUL-1994; U08530. 29-JUL-1993; US-099869. (UNMI ) UNIV MICHIGAN. (TEXA ) UNIV TEXAS SYSTEM. AMMI chromosome inv(16) product.

AMMI; acute myelomonocytic leukemia; chromosinv(16); CBF-beta; CBFB gene; transcription Cobon GS, Austen R Wagland BM; WPI; 89-039628/05. 07-JUL-1987; AU-002940.
(BIOT-) Biotechn Austr Pt, (CSIR) Commonwealth Cobon GS, Austen RA, O'Donnell IJ, Frenkel MJ, Claxton D, 09-FEB-1995. Peptide Key SMMHC. 01-SEP-1995 (first entry) R66930 R66930 standard; Homo sapiens. 356 label= 71 LQNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLAD 400 95-082178/11. leekekkvqeaeaevaalnrrmtlleeeleraeerlkiateklee CBFB 18; 17.1%; Similarity 17.1%; Collins FS, 320 AA; Conservative Location/Qualifiers 1..164 165..885 Protein; Liu 885 Score 128; DB 1; Pred. No. 1.63e-01; 35; Mismatches 49 ď B Siciliano chromosome-16; ription factor; Ŋ, 49; Sci and Kennedy Length Indels 115 inversion, myosin; M d to and WPK, provide pigs be used ψ. Res Orgn. , Savin KW Gaps 70 ţ

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Listing for Mary Hale 4

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R66930).

Probes based on inv(16)

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2-SEP-1986; JP-223972.

09-SEP-1987; JP-223972.

(TOFU) Toa Nenryo Kogyo K

Shida H, Funahashi S;

WPI; 88-086185/13.
                                                                                                                                Disclosure; 3-10; 24pp; English.

The gene is nonessential for proliferation of poxvirus and is homologous with a corresp. gene of a vaccinia virus and can therefore be used for construction of a recombinant vaccinia virus for use as vaccines. The promoter present upstream of this gene is very strong and is adequate as promoter for expression of an exogenous antigen cell.

Sequence 1284 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT 6
P81187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence encoded by a gene fragment coding for major protein of an A-type inclusion body and a promoter region in poxvirus vaccinia virus; vaccine.
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                                                                                                                                                                                                                                                                                                                                                  as vaccines
                                                                                                                                                                                                                                                                                                                                                                                 Gene fragment coding A-type inclusion body in pox virus - used in the construction of recombinant vaccinia viruses for use
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3.0%;
Local Similarity 22.4%;
nes 22; Conservation
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Pred. No. 1.17e-01.
38; Mismatches 5:
            Score 125; DB 1;
Pred. No. 2.66e-01;
35; Mismatches 36
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  Peptide
/label=
                                                                                                 Membrane antigen peptide of human Membrane antigen peptide; human sp diagnosis of infertility; immunisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUL-1987; AU-002940.
(BIOT-) Biotechn Austr Pt, (CSIR)
Cobon CS, Austen RA, O'Donnell IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protective immunity against nematode parasites Claim 5; page 40; 57pp; English.
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                                                         Key
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R51227 standard; Protein;
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                                                                             Homo sapiens.
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larity 21.6%;
Conservative
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                                                                                                         of human sperm; co; human sperm; co; immunisation.
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Pred. No. 8.2
39; Mismatch
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8.27e-01; 75;
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                                                                                                                                      contraceptive vaccine;
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Kennedy
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WPK, Savin KW,
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밁 δ 망 S Matches Query Match Best Local : J06070775-A.
15-MAR-1994
27-AUG-1992; JP-228449
27-AUG-1992; JP-2284
(ISJJ) ISOJIMA S.
WFI; 94-128676/16.
N-PSDB; Q45175. precursor cells
Disclosure; Page 31-32; 43pp; English.
Disclosure; Page 31-32; 43pp; English.
A rat bladder carcinoma cell line 804G (ATCC CRI 11555) protein (150 kDa) includes the sequence given in R63680. The protein stimulates cell adhesion and hemidesmosome assembly, causing cells to grow in a tissue-like fashion. A specific application is the generation of insulin-secreting islet cells suitable for transplantation. The rat matrix protein shows 21% identity to amino acids 1634-1970 of Article for in vivo use coated with protein promoting hemi-desmosome formation — and cellular adhesion, e.g. for prepnof skin allografts, coating prostheses and growing endocrine Membrane antigen peptide of human sperm and a contraceptive vaccine and for diagnosis of Claim 1, Page 8-9; 10pp; Japanese.

R5127 showes the antigen peptide for a monc 06-MAY-1995 (first entry) Merosin amino acids 1634-1970. Jones JCR, Quaranta V; WPI; 94-333178/41. 05-APR-1994; U03733. 05-APR-1993; US-042727. 12-NOV-1993; US-152460. diabetes; merosin; laminin-A. Hemidesmosome; bladder carcinoma; 804G; matrix protein; cell adhesion; skin; allograft; prosthesis; endocrine; islet; pancreas; insulin; R63681 standard; diagnosis of fertilisation. Sequence WO9423016-A. Homo sapiens. Sequence R51227 showes the antigen peptide for a monoclonal antibody immobility action of human sperm and inhibitory action of fertilisation. It is useful for a contraception vaccine and numan meros: (DESM-) DESMOS INC. 272 KVSL-LQNESVEKNKSIQSLHNQICSFEIEIERQKEM-LRNNESKILHLQR-VIDSQAEK 329 LKELDKEIRPF-RONWEEADSMKSSVESLONRVTELESVDKSAGO 245 -sdlerqlktltkqmkeeteewrrfqadlqtavvvandi-kceaq 186 rtslklqekasesdaeikdmketifeledqveqhravklhnnql-iselessvikleeqk 244 2.8%; Local Similarity 24.8%; les 26; Conservative 337 334 AA; JP-228449. 228449 (R63681), a laminin A isoform. peptide; 337 Score 116; DB 10; Pred. No. 1.14e+00; 32; Mismatches 40 B of. its coding f infertility 40; Length Indels 287 372 - used and for the 7; having İ'n Gaps

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membrane

antigen

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Page 9

RESULT IRESULT OF THE SOLUTION 덩 В 8 В Q 밁 δ S 밁 Query Match Best Local S Matches 2 Query Best I Matches SacUS1 confers DegS ph SalI-SphI SacU locus. in microogansisms Claim 3; fig. 5; 87pp; French. Kunst F, Debarbouille M, Msadek T, Rapoport G, WPI; 89-309530/42. P90994; 23-FEB-1990 Sequence microorgansisms. DNA contg. Bacillus subtilis sacU N-PSDB; N91619 22-MAR-1988; FR-0037 (INSP) Inst Pasteur. 22-MAR-1989; 05-OCT-1989. WO8909264-A. Bacillus subtilis. Levan P90994 standard; 168 109 266 381 250 325 190 130 Local cUS1 confers DegS phenotype, and is encoded by part of the 2.55 kb lI-SphI SacU locus. This can restore levan saccharase synthesis in subtilis sacU- mutants, and overproduces proteins in this or other Match subtilis sacUS1 dfgl-riieaqeeerkrvsreih 189 : | |:|::| | | : :||: -LHLQRVIDSQAEKIKELDKEIR 337 aeallkkvkklfgesrgeneemekdlrekladyknkvddawdllreatdkireanrlfav 189 grekglrerrddlerrilglg-eiierseslvsgitvvlnylngldrevgllladagakg 167 ESQLS-RHDQM-LSVHDIRLADM 401 seelndkiddlsqeikdrklaek 272 QAEKLKEIDKEIRPF-RQNWEEADSMKSSVESL-Q-NRVT-ELESVDKSAGQVARNTGLL 380 nqknmtalekkkeavesgkrqientlkegndildeanrladeinsiidyvediqtklppm 249 SNSLEKKVSLLQNESVEKNKSIQ-SLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDS 324 QHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLHNQICSFEIEIERQKEML-RNNESKI 315 saccharase Similarity Similarity 27; Conse 22; 385 AA; 2.8%; larity 18.9%; Conservative FR-003736 Conservative (first entry) protein; 2.8%; polypeptide 385 Pred. 47; N Score 117; DB 1; Pred. No. 9.71e-01; Score 30; Ą e 117; DB 11; Le 1. No. 9.71e-01; Mismatches locus 1 for inducing overproduction 27; Length 385; Klier A, Dedonder Length Indels 4; 7; Gaps Gaps Ŗ

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KW H R43563 standa R43563; 05-APR-1994 Hyaluronan receptor. Hyaluronan binding p standard; (first entry) Protein; protein; HA; RHAMM; mediated motility; Acres A 4 

RESULT

DE AC

Portion

of.

peptide

antigen to malarial sporozite

(first entry)

R05766 stand R05766; R05766; 05-NOV-1990

standard;

protein;

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PS Claim 7; Fig 23; 88pp; English.

CC The sequence is that encoded by a cDNA clone encoding the hyaluronan creeptor (HARC). The sequence was obtd. by screening a 3T3 library in Creeptor (HARC). The sequence was obtd. by screening a 3T3 library in CC lambda gtll with antibodies to HARC. A clone of 1.9 kb was obtained CC clone. HA is down regulated in stationary normal cells and is only CC expressed in situations where cell motility is desired, e.g. in CC wound healing, in response to growth factors and in chemotaxis by white blood cells. HA may be used for diagnosis and treatment of CC white blood cells. HA may be used for diagnosis and treatment of CC diseases involving cell locomotion, e.g. tumour invasion, birth CC defects, acute and chronic inflammatory disorders, Alzheimer; s and CC dysplasias and hypertrophies, burns, surgical incisions and adhesions, CC dysplasias and hypertrophies, burns, surgical incisions and adhesions, CC and spinal cord regeneration, contraception, in vitro fertilisation and CC dysplasias cord pain states involving nerve sprouting; also in CNJ cembrus development Listing for Mary Hale healing; diagnosis; treatment; cell locomotion; tumour invasion; birth defects; inflammatory disorder; Alzheimer's disease; dementia; Parkinson's disease; Huntington's disease; AIDS; auto; immune disease; corneal dysplasia; hypertrophy; surgery; burns; strokes; multiple sclerosis; depression; schizophrenia; CNJ; contraception; in vitro fertilisation; embryo development. 09-APR-1992; GB-007949. (MANI-) MANITOBA CANCER DNA encoding hyaluronan receptor - used to pantibodies for alteration of cell locomotion Turley EA; WPI; 93-351722/44. wo9321312-A. N-PSDB; Q51212. MANITOBA (UYMA-) UNIV. CA0158. GB-007949. TREATMENT Tue & RES FOUND used to produce proteins Mar 19 À 12:36:56 1996 Page 6

S B õ DЬ Ó В Matches Query Match Best Local 378 160 260 NLLKEWSNSLEKKVS-LLQNESVEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHL 101 nllrekevelekhiarqaqailiaqekyidtaqs-lrvvtaqlesvqekyndtaqslrdv 159 GLIESQLSRH-DQMLS-VHDIRLADMDL rdvsaqlesyksstlkeiedlklenltl 247 QRVIDSQAEKLKELDKEIRPFRQNWE-EADSMKSSVESLQNRVTELESVDKSAGQVARNT Similarity
31; Conser 2.8%; larity 20.9%; Conservative Score 118; DB 8; Le Pred. No. 8.27e-01; Mismatches 71; 403 Length 476; Indels 5, Gaps 318 377 5;

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embryo development. See also R46548-51.

Sequence

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S 멍 S 멍 Ś 밁 Query Match Best Local ILT 13
 P90954 standard; |
 P90954;
 P90954;
 27-Feb-1990 (fire Disclosure; fig. 6; 28pp; English. The cDN of this can be spliced into hosts for high yield. This has high Sequence 769 AA; (BRIG) Brigham and Women's Hospital; Earnshaw WC, D'Arpa P; WPI; 89-309500/42. Saccharomyces cerevisiae WO8909222-A. Novel malarial sporozoite useful as vaccine against 22-MAR-1989; U01116. 23-MAR-1988; US-172159. Scleroderma. Yeast topoisomerase Sequence sporozite. Antigen, preferably tetanus toxoid, may Disclosure; p; English parasites. N-PSDB; Q05140. Hollindale MR; (BIOM-) Biomedical Res Inst. 30-NOV-1988; 30-NOV-1989; 005335. 14-JUN-1990 WO9006130-A. Plasmodium falciparum. tetanus 30-NOV-1988; US-278234. 12-APR-1989; US-337204. 262 204 384 321 327 269 Local errakeklqeqqrdleqerlakeklq 346 LSRHDQMLSVHDIRLADMDLGFQVLE 409 90-209624/27. EKLKELDKE-I-RP-FRONWEEADSMKSSVESLONRVTELESVDKSAGQVARNTGLLESO Similarity 32; Conse toxoid 462 AA; (first Conservative protein; 769 2.7%; entry) linked at the C-terminal to a carrier such be used as a vaccine against the malarial antigenic protein
sporozoite(s) and Score Pred. 46; M \$ e 114; DB 1; Len 1. No. 1.57e+00; 1. No. 60; (UYJO) John's Hopkins Univ exoerythrocytic Length 462, useful for large 8 Gaps

Query Malaria; Match eqqsdleqdrlakeklqvqqsdlertkastetlqerqsdleqerrakeklqeqqsdle-q 320 sporozite; vaccine; 2.7%; A 2 Score exoerythrocytic parasites; 111; DNA vectors and used to transform homology with human topoisomerase DB . ۲. Length 769 383 scale æ

> Listing for Mary Hale

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Best Local Similarity 26.4%;
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LT 15
R15148 standard; Protein;
R15148;
14-FEB-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                virus-6 infections
Claim 1; Page 12; 25pp; English.
Claim 1; Page 12; 25pp; English.
This sequence is the pl00 protein from human herpes virus type6.
The protein and antibodies to it can be used for treatment or prevention of HHV-6 infections. The DNA, protein and Ab are also useful in eq. ELISA assays esp. for differentiating between HHV-6 and cytomegalovirus infections. These assays are more sensitive and specific than immunofluorescence methods currently used.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human herpes virus type 6 protein p100 DNA sequence — useful in prophylaxis, treatment and differential diagnosis of human herpes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-1992; 110047.
08-JUL-1991; EP-111338
(BEHW ) BEHRINGWERKE A
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R30729 standard;
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Page 13

A CDNA library (from human thymus mRNA) in lambda gtl1 was screened with serum from a patient having systemic lupus erythematosus. Two clones were reactive with sera (from a panel of lupus patients) which contd. autoantibodies against 52 kD protein.

Both the cDNA and the protein expressed from it, or portions of it, are useful as diagnostic agents in the identification of patients having autoantibodies and in the identification and analysis of the structural and functional properties of the autoantigen and for application in immunotherapeutic regimens. DNA encoding an Ro-SSA autoantigen – useful for diagnosing auto-immune disorders or presence of auto-antibodies Disclosure; Fig 2; 41pp; English. A cDNA library (from human thymus mRNA) in lambda gtll was N-PSDB; Q14798. Frank MB, Itoh K; WPI; 91-353712/48. 07-MAY-1990; US-520270 14-NOV-1991. 07-MAY-1991; U03139. Homo sapiens. WO9117171-A. Autoantibody; autoantigen; SLE; systemic lupus erythematosus Ro/SSA autoantigen. (OKLA-) OKLAHOMA MED RES FO Ŗ

δ 밁 Query Match Best Local S Matches 1 h 2.6%; Similarity 27.3%; 12; Conservative Score 107; DB 3; Pred. No. 4.70e+00; 13; Mismatches 19 19; Length 475; Inde1s ç Gaps

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Search completed: Tue Mar 19 09:53:45 1996 Job time: 28 secs.

(MT)

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Tue Mar 19 09:52:04 1996; MasPar time 18.51 Seconds 773.963 Million cell updates/sec

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Listing for Mary Hale

Tue Mar 19 12:36:56 1996

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Description: Perfect Score: (1-567) from US08404832.pep 4162

Sequence: 1 MESSKKMDSPGALQTNPPIK.....IKDDTIFIKVIVDTSDLPDP 567

Scoring table: PAM 150 Gap 11

Searched: 82306 seqs, 25270970 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

pir46 1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4 8:unann5 9:unann6 10:unann7 11:unann8 12:unrev1 13:unrev2

Statistics: Mean 49.231; Variance 140.106; scale 0.351

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result			,					
4139 99.4 568 11 A55649 TNFR-associated prot 812 19.5 416 11 B55649 DC17 protein - slime 9 164 43.9 46.5 11 A40195 meprin A (EC 3.4.24.14.14.9 3.6 283 5 A60364 tropomyosin - migrat 151 3.6 377 11 A47380 RIMG finger-contain 2 151 3.6 1969 2 S02771 myosin heavy chain A 145 3.5 1959 2 A33977 myosin heavy chain A 145 3.5 1959 2 A33977 myosin heavy chain B 132 3.2 284 5 S24972 myosin heavy chain B 132 3.2 704 11 S3964 mposin heavy chain B 132 3.2 704 11 S3964 print A (EC 3.4.24.2 11 S3964) myosin heavy chain B 133 3.2 704 11 S3964 print A (EC 3.4.24.2 11 S3964) myosin heavy chain B 135 3.2 704 12 S3964 print A (EC 3.4.24.2 11 S3964) mposin heavy chain B 135 3.2 704 12 S3964 print A (EC 3.4.24.2 11 S3964) prin	Result	Score	Query Match		BB	ID	Description	
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RESULT ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE SUMMARY Query Match Best Local Similarity #journal #title #accession **fauthors** ##status prel: ##molecule\_type mRNA ##residues 1-41 ##residus 1-416 ##label MOS ##cross-references GB:U19261 ##cross-references GB:U19261 Mosialos, G.; Birkenbach, M.; Yalamanchili, R.; VanArsdal T.; Ware, C.; Kieff, E. Cell (1995) 80:389-399 The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for the tumor necrosis factor recept family. B55649 B55649 #type complete
TNFR-associated protein EBI6 - human
#formal name Homo sapiens #common name man
23-Mar-1995 #sequence\_revision 23-Mar-1995
23-Mar-1995 A55649 preliminary 19.5%; Score 812; DB 11; Pred. No. 2.29e-93; Length 416; #text\_change factor receptor R.; VanArsdale, 6815



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KEYWORDS SUMMARY ACCESSIONS REFERENCE RESULT ENTRY TITLE D δõ 밁 밁 S В 6 В S В Š Ś Ś DЬ 8 밁 ORGANI SM Query Match Best Local : Matches #authors Driscoll, D.M.; Williams, J.G.
#journal Mol. Cell. Biol. (1987) 7:4482-4489
#title Two divergently transcribed genes of Dictyostelium discoideum are cyclic AMP-inducible and coregulated during development.
#cross-references MID:88142840
#accession A29361 #accession A29361 ##molecule\_type DNA ##residues 1-4 273 448 130 177 179 118 508 359 300 388 240 329 187 213 LRSELSAHLSECVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKK 272 71 idafrpdlssasfqrpqsetnvasgcplffplsklqspkhayvkddtmflkcivets 415
|||:|| :|:|| :| :| ||:|| :| :| :|:||||:||
GDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQTVLENG--TYIKDDTIFIKVIVDTS 562 RNESRGCAEQLMIGHI-VHIKNDCHFEELPCVRPDCKEKVIRKDIRDHVEKACKYREATC 176 SHCK-SQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHL-SECVNAPSTCSFK 234 VS-LLQNESVEKNKSIQSLHNQICSFEIEIERQKEMLKN--NESKI-LHLQRVIDSQAEK 328 lgcglesgpmaleqnlsdlqlqa-avevagdlevdcyrapcsesqeelalqhfmk-e-kl 186 139; 4.6%;
Similarity 25.8%;
39; Conservative A29361 #type complete
DG17 protein - slime mold (Dictyostelium discoideum)
#formal name Dictyostelium discoideum
31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change
31-Dec-1993 - 1-458 ##label DRI DNA binding; zinc finger #length 458 #molecular-weight 53015 #checksum Conservative Score 191; DB 9; Le Pred. No. 9.46e-09; 36; Mismatches 65; 93; Mismatches 106; Length 458; Indels 11; Gaps 10; Indels 19; Gaps 16;

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Q	Db	Qy	Db	Qu Be Mai	87-2 276- SUMMARY	1 - 33 34 - 7 78 - 7	CLAS	***	# # 5		***	*	***	ACCES REFEI	RESULT ENTRY TITLE ALTERNATION ORGANISM DATE
478 RGEYDI	504 agdnda		447 vwtir	ery Match st Local Sir cches 27,	87-273 276-445 MARY	1-33 34-77 78-760	##residues ##residues ##cross-re CLASSIFICATION	#title #cross-referencession	#authors #journal	##Cross-re ##note	accession ##molecule ##residues	ross-refer	#journal #title	ACCESSIONS REFERENCE #authors	RESULT 4 ENTRY TITLE ALTERNATE NAMES ORGANISM DATE
RGEYDALLPWPFKQKVTLM-LMDQGSSRRH 506	sgdndailewpvenrqaimtildqeadtrn 533		nisqilentvkgdkl-v-sprfynse-gygvgvtlypngritsnsgllgltfhly 503	Query Match 3.9%; Score 164; DB 11; Length 760; Best Local Similarity 30.0%; Pred. No. 1.10e-05; Matches 27; Conservative 25; Mismatches 34; Indels 4; Gaps 4;	#domain astacin homology #label AST\ #domain MAM homology #label MAM #length 760 #molecular-weight 85702 #checksum 4733	#domain signal sequence #status predicted #label SIG\ #domain propeptide #status predicted #label PRO\ #product meprin A alpha chain #status experimental #label MAT\	##motectie type mxwA ##residues 77-275 ##label DUM ##cross-references GB:M74897; GB:M74238 #TICATION #superfamily astacin homology; MAM homology	The astacin family of metalloendopeptidases. ences MUID:92042028 B4115-500	Hauthors Dumermuth, E.; Sterchi, E.E.; Jiang, W.; Wolz, R.L.; Bond, J.S.; Flannery, A.V.; Beynon, R.J.  Journal J. Biol. Chem. (1991) 266:21381-21385	ferenc	ession A40195 #molecule_type_mRNA #residues1-760 ##label_JIA	sequencing, differential expression in indred mouse strains, and evidence for divergent evolution of the alpha and beta subunits.  'cross-references MUID:92250517	J. Biol. Chem. (1992) 267:9185-9193 The alpha subunit of meprin A. Molecular cloning and	A40195; B41196 A40195 Jiang, W.; Gorbea, C.M.; Flannery, A.V.; Beynon, R.J.; Grant,	A40195 #type complete meprin A (EC 3.4.24.18) alpha chain precursor - mouse endopeptidase-2 #formal name Mus musculus #common name house mouse 16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change 23-Mar-1995

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Query Match Best Local Sin Matches 24;	ARY ######	#authors Lov O T #journal Pro #title Ide #tross-references	RESULT 6 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE	Db 71 leekek  ::: Qy 356 LQNRVI	Db 13 lekdna :  : Qy 297 FEIEIE	Query Match Best Local Sin Matches 20;	#journal #title #accession #accession ##status ##molecule CLASSIFICATION KEYWORDS SUMMARY	RESULT 5 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors
1 3.6%; Score 151; DB 11; Length 377; Similarity 24.7%; Pred. No. 2.84e-04; Conservative 30; Mismatches 39; Indels 4; Gaps	#SEAU A4/700 #SEAU Preliminary #ROJECULE_Type DNA; protein #rosidues 1-377 ##Jabel LOV #CROSS-references NCBIN:128010; NCBIP:128011 #CROSS-references NCBIN:128010; NCBIP:128011 #CROSS-references NCBIN:128010; NCBIP:128011 #CROSS-references NCBIN:128010; NCBIP:128011 #CROSS-references NCBIP:128010 #CROSS-REFERENCE PROTECTION NCBIP:128011 ##CROSS-REFERENCE PROTECTION NCBIP:128011 ###CROSS-REFERENCE PROTECTION NCBIP:128011 ###################################	ering, R.; Hanson, I.M.; Borden, K.L.; Martin, S.; 'Railly, N.J.; Evan, G.I.; Rahman, D.; Pappin, D.J rowsdale, J.; Freemont, P.S. c. Natl. Acad. Sci. U.S.A. (1993) 90:2112-2116 ntification and preliminary characterization of a otif related to the zinc finger.  MUDD:93211912	A47380 #type complete RING finger-containing DNA binding protein RING1 - human #formal name Homo sapiens #common name man 21-Jan-T994 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994 A47380 A47380	<pre>leekekalqnaesevaalnrriqlleedlerseerlatataklae 115  :::  :: :                            </pre>	lekdnaldrallceqqardan1-ra-ekaeeearalqkkiqtiendldqtqeslgqvmak :  : :  : :: :  :   :   :   : : : : : :	3.6%; Score 149; DB 5; Length 283; Similarity 19.0%; Pred. No. 4.63e-04; 20; Conservative 36; Mismatches 46; Indels 3; Gaps	Hreer, Insect B: Insect B: Cloning, A60364 not le_type_mRNJ es	Tio' H M
4.		protein	e n		70 355	s 3;	ín.	locust

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#authors

#journal #title

Dibb, N.J.; Maruyama, I.N.; Krause, M.; Karn, J. J. Mol. Biol. (1989) 205:603-613 Sequence analysis of the complete Caenorhabditis elegans

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Best Local Similarity 28.9%;
Matches 26; Conservative
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#title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cross-references MUID:92371675
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|: | :| | :| ::| ::| : |:
478 RGEYDALLPWPFKQKVTLM-LMDQGSSRRH 506
                                                                                                                                                                                                                                                                                                           436 vwtirnisqvlentvkgdrl-v-sprfynse-gygfgvtlypngritsnsgylglafhly 492
                                                                                                                                                                                                                                                                            418 IMKIRDYKRRKQEAVMCKTLSLYSQPFYTGYFGYKMCARVYLNGDGMCKGTHLSLFFVIM 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 NCCKREILALQIY-CRNESRGCAEQLMLGHLVHLKND 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 dp-nfdaliskiypsreeyeahqdrvli-rlsrlhnq 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corbeil, D.; Gaudoux, F.; Wainwright, S.; Ingram, J.; Kenny, A.J.; Boileau, G.; Crine, P.
FEBS Lett. (1992) 309:203-208
Molecular cloning of the alpha-subunit of rat
endopeptidase-24.18 (endopeptidase-2) and co-localization
with endopeptidase-24.11 in rat kidney by in situ
hybridization.
                              myosin Affrase (EC 3.6.1.32)

#formal name Caenorhabditis elegans

#formal name Caenorhabditis elegans

31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S24134 #type complete endopeptidase 2 (EC 3.4.24.-) - rat endopeptidase 24.18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-748 ##label COR hydrolase; metalloprotein; proteinase; zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #formal name Rattus norvegicus #common name Norway rat 02-Dec-I993 #sequence_revision 01-Sep-I995 #text_change 01-Sep-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                  #binding_site_zinc (His) #status predicted #length 748 #molecular-weight 85138 #checksum
                    27-Jan-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary
                                                                                                                                                                                                                                                                                                                                                      Score 151; DB 11; Length 748; Pred. No. 2.84e-04; 23; Mismatches 37; Indels
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myosin heavy chain #cross-references MUID:89178677 #accession \$02771 ##residues 1-1969 ##label ##cross-references EMBL:X08067 ##molecule\_type DNA ##residues 1-1: gene family.

#introns CLASSIFICATION GENETICS #gene ##note the nucleotide sequence is not given

KEYWORDS \*superfamily myosin heavy chain; myosin head homology actin binding; ATP; coiled coil; hydrolase; methylation; muscle contraction; tandem repeat 116/3; 169/1; 269/1; 445/2; 1898/3

SUMMARY 185 707,717 770-784 852-1969 852-1166 1167-1969 179-186 667-689 130 #length 1969 #active #binding\_site ATP (Lys) #status predicted) #region nucleotide-binding motif A (P-loop)\
#region actin-binding #status predicted\
#region actin-binding #status predicted\
#comain coiled coil #status predicted #label #domain myosin head homology #label #region light meromyosin\ #modified\_site N6,N6,N6-trimethyllysine (Lys) #status region S2\ predicted\ site Cys #status predict #molecular-weight 225508 #checksum COI/ 6892

Matches Query Match Best Local 3.6%; Similarity 21.2%; 28; Conservation 49; Score 151; DB 2; Pred. No. 2.84e-04; Mismatches 47; Length 1969; Indels Gaps

Ś В 270 EKKVSLLQNESVEKNKSIQSLHNQICSFEIEIERQ-KEMLRNNESKILHLQRVIDSQAEK 328 985 dhnirølqdemanqdeavaklnkek-khqeesnrklnedlqseedkvnhlekirnkleqq 1043

Ś DЬ 329 LKELDKEIRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQVARNTGLLESQLSRHD 388

Вb 1098 edlhhtnaklae 1109

S 389 QMLSVHDIRLAD 400

RESULT ENTRY ACCESSIONS REFERENCE ORGANISM TITLE #journal #title #accession ##status authors \*\*\*molecule\_type mRNA 9 A44980 #type complete
tropomyosin, obliquely striated muscle - nematode
(Trichostrongylus colubriformis)
#formal name Trichostrongylus colubriformis
28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change A44980 Frenkel, M.J.; Savin, K.W.; Bakker, R.E.; Ward, C.W. Mol. Biochem. Parasitol. (1989) 37:191-199 Characterization of cDNA clones coding for muscle tropomyosin of the nematode Trichostrongylus colubriformis. A44980 A44980 12-Apr-1995

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180 694,704 SUMMARY FEATURE 84-764 ACCESSIONS REFERENCE CONTAINS ORGANISM RESULT D В CLASSIFICATION SUMMARY TITLE S 뮹 Ś δ KEYWORDS CLASSIFICATION Matches Query Match Best Local Query Match 174-181 552-565 626-640 837-1936 837-1277 1278-1959 1937-1959 vertebrate cellular myosin. #title #journal 125 accession authors ##residues 1-203.".-..
##cross-references GB:J04669
IFICATION #superfamily tropomyosin
RY #length 284 #molecular-weight 33150 1: 407 VL 347 DSMKSSVESLQNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLGFQ 287 IQSLHNQICSFEIEIERQKEMLKNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEA 346 ##cross-references GB:M26510 ##residues ##molecule\_type mRNA 199 vv 142 ntieaqlkeaq-mlae-ea-drkydevarklamveadleraeeraeagenkiveleeelr 198 85 vaalnrrmtlleeeleraeerlkiatekleeathnvd-eservrkv-menrsfqde-era 141 10 200 408 3.5%; Similarity 21.3%; Shohet, R.V.; Conti, M.A.; Kawamoto, S.; Preston, Y.A.; Brill, D.A.; Adelstein, R.S. Proc. Natl. Acad. Sci. U.S.A. (1989) 86:7726-7730 Cloning of the cDNA encoding the myosin heavy chain of a A33977 #type complete
myosin heavy chain, cellular - chicken
myosin harase (EC 3.6.1.32)
#formal\_name Gallus gallus #common\_name chicken
31-Dec-1993 #text\_change #superfamily myosin heavy chain; myosin head homology
actin binding; ATP; coiled coil; hydrolase; methylation; #length 1959 A33977 A33977 Conservative tandem repeat 27-Jan-1995 1 - 1959#binding\_site ATP (Lys) #status predicted\ #domain myosin head homology #labe! HEA\
#region nucleotide-binding motif A (P-loop)\
#region actin-binding #status predicted\
#region actin-binding #status predicted\ #active #modified\_site N6,N6,N6-trimethyllysine domain carboxyl-terminal #label CBT fregion domain coiled coil #status predicted #label COI\ region light meromyosin\ predicted' 3.5%; ##label SHO site Cys #status predicted #molecular-weight 226502 Score 145; DB 5; Pred. No. 1.23e-03; 49; Mismatches 41; DВ 2; Length 284; Length 1959; #checksum Indels #checksum (Lys) 6. 3641 Gaps #status of a 406 6

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FEATURE 84-764 ACCESSIONS REFERENCE RESULT ENTRY TITLE #map\_position CLASSIFICATION KEYWORDS CONTAINS ORGANISM Ó В δ 밁 б 밁 GENETICS REFERENCE DATE Matches Best Local 174-181 552-565 #authors Saez, C.G.; Myers, J.G.; Shows, T.B.; Leinwand, L.A.
Proc. Natl. Acad. Sci. U.S.A. (1990) 87:1164-1168
#title Human nonmuscle myosin heavy chain mRNA: generation
diversity through alternative polyadenylylation.
#cross-references MUID:90138958 #accession #journal 626-640 gene #accession #authors 1517 1572 dligrdeqneekrkq 1586 415 357 297 ##cross-references GB:M31013 ##cross-references GB:M69180 NCE A34876 ##molecule\_type mRNA ##residues 715-1961 ##label ##residues molecule\_type mRNA GVLIWKIRDYKRRKQ 429 QNRVTELESVDKS-AGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLGFQVLETASYN- 414 FEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESL 356 Similarity 34; Conser GDB:MYH9 22q12.3-q13.1 Simons, M.; Wang, M.; McBride K.; Gdula, D.; Adelstein, R Circ. Res. (1991) 69:530-539 myosin ATPase (EC 3.6.1.32)
#formal name Homo sapiens #common name man
12-May-1994 #sequence\_revision 14-Jul-1994 #text\_ #superfamily myosin heavy chain; myosin head homology
actin binding; ATP; coiled coil; hydrolase; methylation; A61231 Human nonmuscle myosin heavy chains are encoded myosin A61231; A34876 larity 25.2%; Conservative 27-Jan-1995 tandem located on different chromosomes. 1-715 ##label SIM #domain myosin head homology #label HEA\
#region nucleotide-binding motif A (P-loop)\
#region actin-binding #status predicted\
#region actin-binding #status predicted\ domain region domain #type complete heavy chain NMMHC-A, nonmuscle repeat light meromyosin\ coiled coil #status predicted #label Pred. 34; 1 M.; McBride, O.W.; Kawamoto, Adelstein, R.S.; Weir, L. Mismatches SAE No. 1.23e-03; Mismatches 57; Indels 10; S.; Yamakawa, by two genes \_change COI Gaps

837-1938 837-1277 1278-1961 1939-1961 125 modified carboxyl-terminal #label CBT\
cd\_site N6,N6,N6-trimethyllysine 14 (Lys) #status

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FEATURE 87-778 ACCESSIONS REFERENCE CONTAINS ORGANISM ENTRY TITLE б В S В #introns CLASSIFICATION REFERENCE SUMMARY GENETICS KEYWORDS RESULT Matches Query Match Best Local 180 694, 704 177-184 665-687 769-783 851-1966 851-1165 #journal #title #title Periodic charge distributions sequence match cross-bridge #cross-references MUID:82272395 #gene #accession #journal #accession cross-references MUID:83273600 authors .166-1966 authors 1518 gksvhelekskralegqveemktgleeledelgatedaklrl-evnlgamkagfe 1571 1461 yaeerdraeaeareketkalslaraleeameqkaelerlnkqfr-t--emedlmsskddv 1517 ##molecule\_type DNA ##residues 850-1336,'R',1338-1879,'L',1881-1966 ##label ##molecule\_type 357 297 FEIEIERQKEMIRNNESKILHLQRVIDSQAEKIKELDKEIRPFRQNWEEADSMKSSVESL 356 ##cross-references GB:J01050 ##residues 12 QNRVTELESVDKS-AGQVA-RNTGL--LESQL-SRHDQMLSVHDIRLADMDLGFQ 406 h 3.4%; Similarity 27.8%; A93287 Karn, J.; Brenner, S.; Barnett, L. Proc. Natl. Acad. Sci. U.S.A. (1983) 80:4253-4257 Protein structural domains in the Caenorhabditis elegans unc-54 myosin heavy chain gene are not separated by predicted\
 #binding site ATP (Lys) #status predicted\
 #active Site Cys #status predicted
#active Site Cys #status 26741 #checksum unc-54 114/3; 267/1; 528/3; 1750/3; 1822/3; 1897/3 21/3; 64/2; 114/3; 267/1; 528/3; 1750/3; 1822/3; 1897/3 #superfamily myosin heavy chain; myosin head homology actin binding; ATP; coiled coil; hydrolase; methylation; McLachlan, A.D.; Karn, J. Nature (1982) 299:226-231 #formal name Caenorhabdit's elegans 13-Jun-T983 #sequence\_revision 19-Re 27-Jan-1995 MWKW #type complete
myosin heavy chain B - Caenorhabditis elegans
myosin ATPase (EC 3.6.1.32) A93958; A93287; A02992 A93287 Conservative muscle contraction; tandem repeat DNA 1-1966 ##label KAR #domain myosin head homology #label HEA\
#region actin-binding #status predicted\
#region actin-binding #status predicted\ #region domain coiled coil #status light meromyosin\ Score 141; DB 2; Pred. No. 3.21e-03; Mismatches spacings in the myosin 19-Feb-1984 #text\_change 48; predicted #label COI\ Length 1961; Indels μ muscle rod 9; amino 9108 MCL Gaps acid 7;

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183 705, 7 SUMMARY RESULT ENTRY Š 밁 S 밁 CLASSIFICATION SUMMARY RESULT ENTRY 5 밁 б В S 뭣 ORGANISM ACCESSIONS ORGANISM Best Matches Query Match Best Local Matches Query Match #description #submission 128 1097 selhsvssrled 1108 1043 lddledslerekraradldkqkrkveg-elkiaq-enides-gr-qrh-dl-ennlkkke 1096 101 329 289 SLHNQICSFEIEIERQKEMLRNNESKI-LHLQRVIDSQAEKLKELDKEIRPFRQNWEEAD ##molecule\_type mRNA ##residues 1-28 389 270 EKKVSLLQNESVEKNKSIQSLHNQICSFEIEIERQ-KEMLRNNESKILHLQRVIDSQAEK 328 ##cross-references EMBL:X66274 ##status 45 slqkklkatedeldkysealkdaqeklelaekkatdaead-vaslnrriqlf-e--eeld 100 / Match 3.4%; Local Similarity 24.2%; les 32; Conservative , 715 14 SMKSSVESLQNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLAD 400 --raq-erlatalqkleeaekaadesergmkviesraqkdeekmeiqeiqlke 150 QMLSVHDIRLAD 400 LKELDKEIRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQVARNTGLLESQLSRHD 388 h 3.2%; Similarity 23.9%; 12-Apr-1995 \$24972 s33068 #type complete myosin II heavy chain - fluke (Schistosoma mansoni) #formal\_name Schistosoma mansoni Whitby, F.G.; Kent, H.M.; Stewart, F.; Stewart, M.; Hatch, V.; Cohen, C.; Phillips Jr., G. submitted to the EMBL Data Library, April 1992 Structure of tropomyosin at 9 Angstroms resolution. #superfamily tropomyosin
#length 284 #molecular-weight 32729 S24972 S24972 tropomyosin alpha, cardiac - pig #formal name Sus scrofa domestica #common name domestic 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change predicted\
#binding\_site ATP (Lys) #status predicted\
#active\_site Cys #status predicted
#active\_site Cys #status predicted
#active\_site Cys #status predicted
#active\_site Cys #status predicted
#active\_site Cys #status predicted\
#active\_site Cys S24972 Conservative 1-284 ##label WHI preliminary #modified\_site N6,N6,N6-trimethyllysine (Lys) #status #type complete Score 132; DB 5; Pred. No. 2.67e-02; 39; Mismatches 39 Score 142; DB 2; Le Pred. No. 2.53e-03; 37; Mismatches 55; 39; Length 1966; Length 284; Indels #checksum Indels #checksum 8 8 9163 Gaps Gaps Xie, 347 8 6;

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                                                                                                                                                                                                                                                                                                                         authors
                                                                                                                                                                            ##molecule_type mRNA
##residnee
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                                                                                                                                       ##cross-references EMBL:X81333
FICATION #superfamily MAM homology; astacin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 EKKVSLLQNESVEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 1-527 ##label SOI
##cross-references EMBL:X65591
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29; Conservative
h
Similarity 33.3%;
30; Conservative
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Soisson, L.M.A.; Masterson, C.P.; Tom, T.D.; McNal Lowell, G.H.; Strand, M.
J. Immunol. (1992) 149:3612-3620
Induction of protective immunity in mice using a recombinant fragment of a Schistosoma mansoni s
                                                                                                                                                                                                                                                                                                                                     S49383
S49383
                                                                                                                                                                                                                                                                                                                                                                 $49383 #type complete meprin A (EC 3.4.24.18) - human #formal name Homo sapiens #common name man 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 26-May-1995
                                                                                                                                                                                                                                                  Cloning and the PABA-peptide hydrolase beta subunit: coexpression is required for plasma membrane localization of the alpha subunit in COS-1 cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-May-1995
S33068
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                                                                                                                                                                                                                                                                                                 Eldering, J.A.; Groenberg, J.; Sterchi, E.E. submitted to the EMBL Data Library, September 1994
                                                                    #length
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gth 700
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                                                                                                                                                                                                                                                the alpha subunit in COS-1 cells.
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#domain MAM homology #label MAM
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                                                                      *molecular-weight
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Pred. No. 2.67e-02;
33; Mismatches 51;
 Score 132; DB 10; Length 700; Pred. No. 2.67e-02; 20; Mismatches 29; Indels 1
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Tue Mar 19 12:36:57 1996

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Page 27

S Db S Db 478 RGEYDALLPWPFK-QKVTLMIMDQGSSRRH 506 481 sganddqlqwpcpwqqatmtlldqnpdirq 510 418 431 

Search completed: Tue Mar 19 09:52:59 1996 Job time: 55 secs.

(MT)

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Tue Mar 19 09:51:11 1996; MasPar time 10.24 Seconds 848.774 Million cell updates/sec

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Description: Perfect Score:

>US-08-404-832-2 (1-567) from US08404832.pep 162 1 MESSKKMDSPGALQTNPPLK......IKDDTIFIKVIVDTSDLPDP 567

Scoring table: PAM 150 Gap 11

43470 seqs, 15335248 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot31
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8

Statistics: Mean 51.439; Variance 108.497; scale 0.474

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES



Listing for Mary Hale

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4.24e-03 4.24e-03	9	.24e-	7e-0	.24e-0	.67e-0	.16e-0	.24e-0	.57e-0	.67e-0	.67e-	.67e-	.67e-	.67e-	.67e-	246-	.57e-	160-	7 576-03	300	. 36e-	.18e-	. 75e	9.68e-04	.30e	36e-	30e-	.18e-		180	750-	2.14e-04			9.59e-06		1.41e-06		. 98e-	20-12	1 226-122	3	Pred. No.

#### ALIGNMENTS

So	DE	DΤ	DΤ	ΡŢ	AC	Ħ	RESULT
MUS MUSCULUS (MOUSE).	RECEPTOR ASSOC	(REL.	(REL. 31,	1995	29;	TRF2 MOUSE STANDARD; PRT; 501 AA.	SULT 1



EUKARYOTA; EUTHERIA; F [1]

RODENTIA.

CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

A. 18.

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S 밁 Ś B δ 밁 δ В Matches Query Match Best Local SEQUENCE FROM N.A.

94349371

94349371

ROTHE M., WONG S.C., HENZEL W.J., GOEDDEL D.V.;

ROTHE M., WONG S.C., HENZEL W.J., GOEDDEL D.V.;

ROTHE J. WONG S.C., HENZEL W.J., GOEDDEL D.V.;

CELL 78:681-692(1994).

-1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE

-1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE

-1- SUBCELLULAR LOCATION: CYTOPLASMIC.

-1- SUBUNIT: HETERODIMER OF TRAF1 AND TRAF2.

-1- SUBUNIT: GONTAINS A C3HC4-CLASS ZINC FINGER

EMBL; L35303; MATTRAF2A.

ZINC-FINGER; COLLED COLL.

ZINC-FINGER; COLLED COLL.

ZINC-FINGER; COLLED COLL.

ZINC-FINGER; COLLED COLL. 94349371 TRF1 MOUSE STANDARD; PRT; 409 AA. 739428; 01-FEB-1995 (REL. 31, CREATED) 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE) 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE) TOF RECEPTOR ASSOCIATED FACTOR 1 (TRAF1).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; ROTHE M., WONG S.C., HENZEL W.J., GOEDDEL D.V.;
CELL 78:681-692(1994).
-I- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH
OF THE 75 KD TUMOR NECROSIS FACTOR RECEPTOR
-I- SUBCELLULAR LOCATION: CYTOPLASMIC.
-I- SUBUNIT: HETERODIMER OF TRAF1 AND TRAF2. SEQUENCE COLLED EMBL; SEQUENCE FROM N.A., AND SEQUENCE EUTHERIA; RODENTIA. SEQUENCE 496 500 437 440 377 559 VDTSDL vdltgl QGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQTVLE-NGTYIKDDTIFIKVI h-nnrehvidafrpdvtsssfqrpvsdmniasgcplfcpvskmeaknsyvrddaifikai : :| |: || :| || :| || || || || L35302; MMTRAF1A. COIL. Similarity 98; Conser 409 AA; 501 AA; 501 564 Conservative 19.2%; 52.7%; 45464 56026 MW; ¥. 49; Score 798; DB 7; I Pred. No. 5.03e-123; C3HC4-TYPE. 1; 1264825 C1 857796 Mismatches OF 123-135 AND S Ω . FINGER. Length 501; THE CYTOP (TNF-R2). THE CYTOPLASMIC DOMAIN (TNF-R2). 390-402 Indels CYTOPLASMIC DOMAIN 2; Gaps 495 558

1

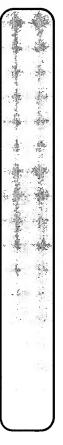
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Listing for Mary Hale 746 Mar 19 12:36:57 1996

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Best Local Similarity
                                                                                                                                                                                                                               BB142840
BB142840
DRISCOLL D.M., WIL
DICTYDB; DD02010; ZFAA.
DEVELOPMENTAL PROTEIN; ZINC
SIMILAR 25 67
ZN FING 27 66
ZN FING 178 198
SEQUENCE 458 AA; 53015 M
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P11467;
01-OCT-1989
01-OCT-1989
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                          DICTYOSTELIUM DISCOIDEUM (SLIME MOLD). EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; EUMYCETOZOA; DICTYOSTELIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                DG17 PROTEIN.
ZFAA OR DG17.
                                                                                                                                             EMBL; M18106; DDDG17A. PIR; A29361; A29361.
                                                                                                                                                                                         DRISCOLL D.M., WILLIAMS J.G.;
MOL. CELL. BIGL. 7:4442-4469(1987).
-i- THE EXPRESSION OF DG17 PROTEIN IS DEVELOPMENTALLY REGULATED.
-i- INDUCTION: BY CAMP DURING AGGREGATION.
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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541 VLENG--TYIKDDTIFIKVIVDTS
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12, LAST SEQUENCE UPDATE)
28, LAST ANNOTATION UPDAT
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No. 1.22e-122;
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                                                                          (AA 71-108).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265
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RNESRGCAEQIMIGHI-VHIKNDCHFEELPCVRPDCKEKVLRKDLRDHVEKACKYREATC 176

Query Match Best Local Matches

39; Similarity

4.6%; larity 25.8%; Conservative

Score Pred. 36; N

e 191; DB 2; Len. .. No. 1.82e-12;

Length 458; Indels 11;

Gaps

### Tue Mar 19 12:36:57

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                                                           PREFERENCE.

-!- COFACTOR: ZINC.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SUBCULTULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SUBUNIT: HOMOTETRAMER OF ALPHA OR BETA SUBUNITS; HETEROTETRAMER OF TWO ALPHA AND TWO BETA SUBUNITS ARE FORED BY NON-COVALENT ASSOCIATION OF TWO DISULFIDE-LINKED HETERODIMERS; GENETIC FACTORS DETERMINE WHICH OLIGOMER(S) WILL BE FORMED (STRAIM-SPECIFIC).

-!- PTM: N-GLYCOSYLATED; AT LEAST 3 OF THE POTENTIAL SITES ARE USED.

-!- PTM: SPECIFICITY: KIDNEY, INTESTINAL BRUSH BORDERS, AND
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P28825;

P28825;

01-DEC-1992 (REL. 24, CREATED)

01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)

01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)

01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DUMERMUTH E., STERCHI E.E., JIANG W., WOLZ R.L., BOND J.S., FLANNERY A.V., BEYNON R.J.;
J. BIOL. CHEM. 266:21381-21385(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6,
92250517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 77-275 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. BIOL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARSTRAIN=C57BL/6, AND C3H/HE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179
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PTM: N-GLYCOSYLATED; AT LEAST TISSUE SPECIFICITY: KIDNEY, SALIVARY DUCTS.
SIMILARITY: HIGH TO OTHER ZI ASTACIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dfckrddikkkelethykt-cpmvpidcsqgcsvk-ierksiidhiendccntqipckyf 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHEM. 267:9185-9193(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARTIAL SEQUENCE
                                      OTHER ZINC METALLOPROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BEYNON
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                                      BELONGS TO
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METAL DISULFID DISULFID TRANSMEM DOMAIN DOMAIN DOMAIN REPEAT CARBOHYD CARBOHYD METAL ACT SITE METAL PIR; A40195; A40195.
PDB; 11AF; 31-AUG-94.
PROSITE; PS00142; ZINC PROTEASE.
PROSITE; PS00740; MAM. EMBL; M74897; EMBL; M82962; DISULFID DOMAIN SIGNAL HYDROLASE; METALLOPROTEASE; ZINC; ZYMOGEN; SIGNAL; EGF-LIKE DOMAIN; -!- SIMILARITY: THE PROTEIN INCLUDES 1
-!- SIMILARITY: CONTAINS A MAM DOMAIN. 688 693 710 41 152 234 270 330 426 452 546 553 614 272 688 699 693 708 693 708 411 41 52 152 34 234 4 234 4 234 4 234 6 270 1 330 452 5456 553 614 272 MW; 34 78 78 727 727 755 755 768 276 685 167 168 171 HSPPH. MMMEPRINA. 760 726 754 760 760 275 275 275 167 167 171 171 BY SIMILARITY.
ZINC (CATALYTIC)
ZINC (CATALYTIC)
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY. POTENTIAL. POTENTIAL. POTENTIAL. EGF-LIKE.
ZINC (CATALYTIC) CYTOPLASMIC (POTENTIAL).
CATALYTIC (ASTACIN DOMAIN). POTENTIAL. MEPRIN A ALPHA-SUBUNIT. EXTRACELLULAR (POTENTIA GLYCOPROTEIN; 3D-STRUCTURE. EGF-LIKE (POTENTIAL). (B) (BY SIMILARITY). REPEAT TRANSMEMBRANE; SIMILARITY) SIMILARITY)

SEDITAC 8 B RESULT TPMM LOCMI STAND
P31816;
01-JUL-1993 (REL. 26
01-JUL-1993 (REL. 26
01-JUL-1993 (REL. 26
TROPOMYSSIN, MUSCLE:
LOCUSTA MIGRATORIA 478 504 sgdndailewpvenrgaimtildgeadtrn 533 RGEYDALLPWPFKQKVTLM-LMDQGSSRRH (REL. 26 (REL. 26 (REL. 26 , MUSCLE. STANDARD; 26, (MIGRATORY LOCUST) CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT PRT; 506 283 A

Ó B

118 IWKIRDYKRKKQEAVMGKTISLYSQEFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIM 447 vwtirnisqilentvkgdkl-v-sprfynse-gygvgvtlypngritsnsgllgltfbly 503 Query Match Best Local S Matches 2

Similarity 27; Conser

3.9%; larity 30.0%; Conservative

Score 164; DB 5; L Pred. No. 1.98e-08; 25; Mismatches 34;

Length 760;

Indels

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Gaps

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2920193 CN;

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CARBOHYD

CONFLICT SEQUENCE



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SEQUENCE FROM N.A.

EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; ORTHOPTERA
[1]

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Listing for Mary Hale

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4;

Gaps

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IRESULT
ACCOMENTATION
RESULT
A SO DE PRESENCE CO CO CE PRESENCE CO CO CO CE PRESENCE PRE S 밁 S 밁 Query Match Best Local : Matches Query Match DOMAIN DOMAIN LOVERING R., HANSON I.M., BORDEN K.L.B., MARTIN S., EVAN G.I., RAHMAN D., PAPPIN D.J.C., TROWEDALE J., F. PROC. NATL. ACAD. SCI. U.S.A. 90:2112-2116(1993).
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER. Q06587; RIN1 PIR; MUSCLE CONTRACTION.
-!- DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQUENCE EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY. KRIEGER J., RAMING K., KNIPPER M., GRAU M., MERTENS S., BREER H.;
INSECT BIOCHEM. 20:173-184(1990).
-i- FUNCTION: TROPOMYOSIN, IN ASSOCIATION WITH THE TROPONIN COMPLEX,
PLAYS A CENTRAL ROLE IN THE CALCIUM DEPENDENT REGULATION OF EMBL; SEQUENCE FROM N.A. 93211912 HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES. 01-JUN-1994 (REL. 01-JUN-1994 (REL. 01-OCT-1994 (REL. SEQUENCE DOMAIN ZINC-FINGER; PROSITE; RING1 PROTEIN SEQUENCE PROSITE; PROSITE; MUSCLE 356 297 71 , Z14000; HSRING1. A47380; A47380. LQNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLAD leekekalqnaesevaalnrriqlleedlerseerlatataklae 115 FEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEA-DSMKSSVES 355 HUMAN A60364; P28990; PROTEIN; 20; h 3.6%; Similarity 19.0%; PS00325; COFILIN TROPOMYOSIN. PS00326; TROPOMYOSIN. PS00518; ZINC FINGER C3HC4.

SER; DNA-BINDING; NUCTEAR PROTEIN.

19 58 C3HC4-TYPE. 377 283 AA; A60364. Conservative 1CHC STANDARD; COILED COIL; 29, 30, 58 231 348 175 32439 MW; 39145 3.6%; CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE) WW. Score 149; DB 7; Le Pred. No. 2.69e-06; 36; Mismatches 46; Score 151; GLY-RICH. GLY-RICH. REPEAT. NUCLEAR LOCALIZATION SIGNAL (POTENTIAL) 716288 CN; C3HC4-TYPE. PRT; 334140 CN; 377 DB A 6 Length 283; Length Indels FREEMONT P.S.; 377; γ, Gaps

ψ RESULT FOR SERVICE OF CC -!- FUNCTION: MUSCLE CONTRACTION.

CC -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

CC HEAVY CHAIN SUBUNITS (MLC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

CC HEAVY CHAIN SUBUNITS (MLC), 2

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

CC -I EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LAM)

CC AND 1 HEAVY MEROMYOSIN (HAM). IT CAN LATTER BE SPLIT FURTHERE INTO

CC 2 GLOBULAR SUBERACHENTS (S1) AND 1 ROD-SHAFED SUBERACHENT (S2).

CC -I DOMAIN: THE RODLIKE TALL SEQUENCE IS HIGHLY REPETITIVE, SHOWING

CC -I CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

CC -I SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.

CC -I SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.

CC -I SUBCELLULAR LOCATION: THE GLOBULAR HEAD SEQUENCE SHOWS A HIGH DEGREE OF

CC SIMILARITY: THE GLOBULAR HEAD SEQUENCE SHOWS A HIGH DEGREE OF

CC SIMILARITY WITH THE GLOBULAR HEAD SEQUENCE IS LESS CONSERVED, BUT

CC HEAVY CHAINS. BY CONTRAST THE ROD SEQUENCE IS LESS CONSERVED, BUT

CC THE PERIODICITIES OF HYDROPHOBIC & CHARGED RESIDUES, WHICH DICTATE

CC -I PINE ALPHA-HELLCAL COILED-COIL STRUCTURE, ARE CONSERVED.

CC -I PINE TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY

CC -I PINE THE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS IN C. ELEGANS.

CC -I HERCA ARD MHC B ARE FOUND EXCLUSIVELY IN THE BODY WALL MUSCLE.

CC -I HERCA ASSEMBLE INTO BODY WALL THICK FILAMENT. S 망 S 밁 Best Matches DOMAIN
NP BIND
DOMAIN
DOMAIN EMBL; DIBB N.J., MARUYAMA I.N., KRAUSE J. MOL. BIOL. 205:603-613(1989).
-!- FUNCTION: MUSCLE CONTRACTION. SEQUENCE FROM N.A. STRAIN=BRISTOL N2; ASYM HSSP; 8917867 CAENORHABDITIS ELEGANS MYOSIN HEAVY 01-OCT-1989 01-OCT-1989 P12844; MULTIGENE FAMILY. DOMAIN 1 NISOYM; EUKARYOTA; METAZOA; MYOSIN; MUSCLE PROTEIN; CO 104 NCCKREILALQIY-CRNESRGCAEQLMLGHLVHLKND 139 Local Similarity hes 24; Conse 11 rslhselmcpicldmlkntmttkeclhrfcsdcivtalrsgnkecptcrkklvskrs1rp 70 ::: :| | :| :| :| :: :: :: 71 dp-nfdaliskiypsreeyeahqdrvli-rlsrlhnq 105 : : : | || || : ::::: :| :| |: 45 KTVEDKYKCEKCHLVLCSPKQT-ECGHRFCESCMAALLSSSSPKCTACQESIVKDKVFKD 103 \$02771; S02771. CAEEL P24733; 1SCM. 852 179 179 667 (REL. 12, CREATED)
(REL. 12, LAST SEQUENCE UPDATE)
(REL. 29, LAST ANNOTATION UPDATE)
(CHAIN A (MHC A). larity 24.7%; Conservative STANDARD; 851 1969 186 689 784 ACOELEMATES; NEMATODA; SECERNENTEA; RHABDITIDA. COILED COIL; 7 Pred. 30; 1 ATP. GLOBULAR HEAD ACTIN-BINDING ACTIN-BINDING PRT; : ; No. 1.41e-06; Mismatches 39; 1969 TAIL KARN THICK FILAMENT; HEPTAD REPEAT 1 AA. (S2 A) ٠<u>.</u> AND 3 Indels PATTERN; ACTIN-BINDING; DOMAINS).



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S 밁 Ś 밁 SOFT Query Match Best Local S Matches 2 MOD\_RES MOD\_RES MOD\_RES SEQUENCE 1044 270 329 985 mdeleenidrekrsrgdiekakrkveg-dlkvaq-enideitkq--kh-dv-ettlkrke 1097 EKKVSLLQNESVEKNKSIQSLHNQICSFEIEIERQ-KEMLRNNESKILHLQRVIDSQAEK 328 IKELDKEIRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQVARNTGLLESQLSRHD 28; 3.6%; Similarity 21.2%; 130 707 717 1969 Conservative Ą, 130 707 717 225509 WW; METHYLATION (TRI-) (ALKYLATION (SH-1) (FALKYLATION (SH-2) (FALKYLATION (SH-2) (FALKYLATION (SH-2)) (FALKYLATION (S 49; Score 151; DB 5; Pred. No. 1.41e-06; Mismatches 47; (POTENTIAL).
(POTENTIAL). Length 1969; Indels 8 Gaps 388

RESULT OI-JAN 1990 (REL. 13, CREATED)
OI-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
OI-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
MYOSIN HEAVY CHAIN, NONMOSCLE (NAMHC).
GALLUS GALLUS (CHICKEN).
GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE; ADELSTEIN R.S.;
PROC. NATL. ACAD. SCI. U.S.A. 86:7726-7730 (1989).
-!- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS, MYSN CH P14105; SEQUENCE FROM N.A.
TISSUE=INTESTINAL EPITHELIUM; SHOHET R.V., GALLIFORMES CHICK CONTI M.A., KAWAMOTO S., STANDARD; PRT; 1959 AA PRESTON Y.A., BRILL D.A.

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edlhhtnaklae 1109

-!- SUBDUTT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LICHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LICHT CHAIN SUBUNITS (MLC-2).
-!- EACH MYOSIN HEAVY CHAIN SUBUNITS (MLC-2).
-!- EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LICHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATTER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRACKENTS (S1) AND 1 ROD-SHAPED SUBFRACKENT (S2).
-!- DOMAIN: THE MODLIKE TAIL SCOUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
-!- SIMILARITY: BELONGS TO THE MYOSIN HEAVY CHAIN FAMILY. STRONGEST TO OTHER NONMUSCLE MYOSINS.
-!- SIMILARITY: BELONGS TO THE MYOSIN HEAVY CHAIN FAMILY. STRONGEST EMBL; M26510; GGMYHN.
-!- RIR; A33977; A33977.
HSSP; P24733; 1SCM.
MYOSIN; COILED COIL; ACTIN-BINDING; ALKYLATION; ATP-BINDING; MEPTAD REPEAT PATTERN; MULTICENE FAMILY.
DOMAIN
1 835 GLOBULAR HEAD (S1).
DOMAIN 836 1926 RODLIKE TAIL (S2 AND LAM DOMAINS). ---!

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MYOSIN; HEPTAD PIR;

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### Listing for I Mary Hale

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Best Local
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01-JUN-1994
01-JUN-1994
MYOSIN HEAVY
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DOMAIN
MOD RES
MOD RES
SEQÜENCE
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                                                                                                                  SEQUENCE
90138958
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                                                                                                                                                                                                                   TOOTHAKER L.E., GONZALEZ D.A., ARNAOUT M.A., CLAYTON L.K., TE BLOOD 78:1826-1833(1991).
                                                                                                                                                                                                                                                                                                                                                                                            P35579;
                                                                                                                                                                                                                                                                                                                                                                                                         NSYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1572 dllgrdegneekrkg 1586
                                                                  SAEZ C.G., MYERS J.C., SHOWS T.B., LEINWAND L.A.;
PROC. NATL. ACAD. SCI. U.S.A. 87:1164-1168 (1990).
-!- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTO
CELL. SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION
                                                                                                                                                 CIRC.
                                                                                                                                                                                                                                                                                                                                   TYPE A) (NMMHC-A).
               <u>:</u>
                                                                                                                                                                          SIMONS
                                                                                                                                                                                     91316803
                                                                                                                                                                                              SEQUENCE OF 1-715 FROM N.A.
                                                                                                                                                                                                                                                                                      HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                  EUKARYOTA;
                                                                                                                                                                                                                                                        92003925
                                                                                                                                                                                                                                                                  SEQUENCE OF 1-1337 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357
                                                                                                                                                                                                                                                                                                                                                                                                                                                   415 GVLIWKIRDYKRRKQ 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 FEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESL
CAPPING.

CAPPING.

SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) CHAIN SUBUNITS (MLC-2).

REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOS AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATTER BE SPLIT FURTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QNRVTELESVDKS-AGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLGFQVLETASYN- 414
                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                  RES.
                                                                                                                                                                      ĭ.
                                                                                                                                                                                                                                                                                                                                             1994 (REL. 29, CREATED)
1994 (REL. 29, LAST SEQUENCE UPDATE)
1994 (REL. 29, LAST ANNOTATION UPDAT
HEAVY CHAIN, NONMUSCLE TYPE A (CELLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 34; Conse
                                                                                                                             OF 715-1961 FROM N.A.
                                                                                                                                                , WANG M., MCBRIDE O.W., ADELSTEIN R.S., WEIR L.; 69:530-539(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174
654
694
704
1959
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larity 25.2%;
Conservative
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ACTIN-BINDING.
ALKYLATION (SH-1)
ALKYLATION (SH-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 145; DB 5; L
Pred. No. 9.59e-06;
34; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW; 15394260
                                                                                                                                                                                                                                TENEN D.G.;
                                                                                                                                                                                                                                                                                                   VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                        KAWAMOTO
                                                                                                                                                                                                                                                                                                                                               ION UPDATE)
A (CELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                       1961
                                                                                                                                                                                                                                           LEMONS
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                                                                                                                                                                                                                                                                                                   TETRAPODA;
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                                                                                                                                                                          YAMAKAWA
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   LIGHT MEROMYOSIN
BE SPLIT FURTHER
                                                                                                                                                                                                                                           s,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 10;
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                                                                                                                                                                                                                                                                                                   MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                HEAVY CHAIN,
                                                                                CYTOKINESIS,
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                                                                                                                                                                                                                                           BEAU M.M.,
                                                                       AND
                                   AND 2
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   OTNI
(MMI)
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RESULT RESULT ACCORDING TO THE PROPERTY OF THE S В б 멍 SO THE THE TENT OF Query Match Best Local S Matches 3 EMBL; M81105; HSMYH9.
EMBL; M69180; HSMYOHCA.
EMBL; M31013; HSMYONM.
HSSP; P24733; ISCM.
MIM; 160775; 11TH EDITION MYSB CAEEL P02566; 1518 CONFLICT CONFLICT CONFLICT CONFLICT CONFLICT SEQUENCE DOMAIN DOMAIN 21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
MYOSIN HEAVY CHAIN B (MHC B).
UNC-54 OR MYO-4. 1461 yaeerdraeaeareketkalslaraleeameqkaelerlnkqfr-t--emedlmsskddv 1517 MYOSIN; + PROC. NATL. ACAD. KARN J., 83273600 EUKARYOTA; METAZOA; ACOELEMATES; CAENORHABDITIS ELEGANS MOD\_RES MOD\_RES DOMAIN NP BIND HEPTAD 297 EQUENCE OF 850-1966 FROM N.A. 2272395 EQUENCE FROM N.A. 2 GLOBUIAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

SIMILARITY: BELONGS TO THE MYOSIN HEAVY CHAIN FAMILY. STRONGEST TO OTHER NONMUSCLE MYOSINS. 10 QNRVTELESVDKS-AGQVA-RNTGL--LESQL-SRHDQMLSVHDIRLADMDLGFQ 406 gksvhelekskraleggveemktgleeledelgatedaklrl-evnlgamkagfe 1571 FEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESL 356 3.4%; Similarity 27.8%; 32; Conservation REPEAT 2775; 11TH EDITION.
COILED COIL; ACTIN-BINDING; ALKYLATION; ATP-BINDING; BRENNER S., BARNETT L.; TL. ACAD. SCI. U.S.A. 80:4253-4257(1983). 53 660 869 931 PATTERN;
1 835
3 1926
336 1926
674 676
694 694
704 704
53 55
660 660
869 869
931 931 STANDARD; AA; 1241 \*\*: 226600 N MULTIGENE ALKYLATION (SH-1) (POTENTIAL).

ALKYLATION (SH-2) (POTENTIAL).

EAI -> RGH (IN REF. 2).

T -> S (IN REF. 2).

T -> M (IN REF. 3).

C -> Y (IN REF. 3).

KG -> GR (IN REF. 3). W. Score 141; DB 5; Pred. No. 3.37e-05; 26; ATP. ACTIN-BINDING. GLOBULAR HEAD (S1). RODLIKE TAIL (S2 AND LMM DOMAINS). Mismatches NEMATODA; SECERNENTEA; RHABDITIDA. 15612344 CN; 1966 AA 48; Length 1961; Indels 9; Gaps

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DЬ Ś В S CC -!- SUBUNIT: MUSCLE WOOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
CC -!- EACH MYOSIN HEAVY CENIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM)
CC AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATTER BE SPLIT FURTHER INTO
CC 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRACENT (S2).
CC -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CC -!- SUBCELIULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
CC -!- SUBCELIULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
CC -!- SIMILARITY HITH THE GLOBULAR HEAD AS SEQUENCE SHOWS A HIGH DEGREE OF
CC SIMILARITY WITH THE GLOBULAR HEAD SEQUENCE SIONS A HIGH DEGREE OF
CC SIMILARITY WITH THE GLOBULAR HEAD SEQUENCE SIONSERVED, BOT
CC THE PERIODICITIES OF HYDROPHOBIC & CHARGED RESIDUES, WHICH DICTATE
CC THE ALFMA-HELICAL COILED-COIL STRUCTURE, ARE CONSERVED,
CC -!- THERE ARE FOUR DIFFERENT MYOSIN ATPASE ACTIVITY.
CC -!- THERE ARE FOUR DIFFERENT MYOSIN ATPASE ACTIVITY.
CC -!- THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS IN C. ELECANS.
CC -!- MHC A AND MHC B ARE FOUND EXCLUSIVELY IN THE BODY WALL MUSCLE.
THEY CO-ASSEMBLE INTO BODY WALL THICK FILAMENT. Query Match Best Local S Matches MOD RES NP BIND WATERSTON R.H.; CELL 33:575-583(1983). -!- FUNCTION: MUSCLE CONTRACTION: CONFLICT EMBL; J01050; CEMYUNC. EMBL; V01494; CEMY01. PIR; A02992; MWKW. SEQUENCE OF 83232892 MYOSÍN; MUSCÍE PROTEIN; COILED COIL; THICK FILAMENT; ACTIN-BINDING; ATP-BINDING; METHYLATION; ALKYLATION; HEPTAD REPEAT PATTERN; WILLS N., SEQUENCE DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN MULTIGENE FAMILY. ATP-BINDING; METHYLATION; 984 dhqirslqdemqqqdeaiaklnkek-khqeeinrklmedlqseedkgnhqnkvkakleqt 1042 270 EKKVSLLQNESVEKNKSIQSLHNQICSFEIEIERQ-KEMLRNNESKILHLQRVIDSQAEK 328 P02649; 1LE4. h 3.4%; Similarity 24.2%; 32; Conservative GESTELAND R.F., 850 1165 177 665 769 128 705 1876-1966 FROM N.A. AA; 849 1966 11164 1966 184 687 783 128 705 715 715 1880 225125 MW; KARN J., BARNETT L., BOLTEN S., Pred. 37; 1 HINGE. E -> R (IN REF. 2). I -> L (IN REF. 2). MW; 15251009 CN; Score 142; DB 5; Pred. No. 2.46e-05; RODLIKE TAIL (S2 AND LMM DOMAINS). ALPHA-HELICAL TAILPIECE (S2). LIGHT MEROMYOSIN (LMM). ALKYLATION (SH-2). METHYLATION (TRI-) ALKYLATION (SH-1). ACTIN-BINDING. ATP (BY SIMILARITY) GLOBULAR HEAD ACTIN-BINDING Mismatches (S1) 55; Length 1966; (POTENTIAL). Indels 8 Gaps



NATURE 299:226-231(1982). [3]

MCLACHLAN A.D.,

KARN J.;

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Gaps

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CONSERVED.

CONSERVED.

-!- PTM: TWO CYSTEINE RESIDUES IN
ALKYLATED AND ARE REQUIRED FO
EMBL; X06546; GGMYHGSM.
PIR; S03166; S03166. YANAGA MASAKI T.; MOL. BIOL. -i- SUBDINIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MLC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-i- EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM)
AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATTER BE SPLIT FURTHER INTO
2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).

-i- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS
-i- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
-i- SUBCELLULAR TOTALE PERIODICITIES OF THE MYOFIBRILS.
-i- SUBCELLULAR TOTALE PERIODICITIES OF THE MYOFIBRILS.
-i- SUBCELLULAR TOTALE PERIODICITIES OF THE MYOFIBRILS. NP\_BIND DOMAIN DOMAIN MOD\_RES REVISIONS.
MASAKI T.; 01-JAN-1990 (REL. 13, LA 01-JUN-1994 (REL. 29, LA MYOSIN HEAVY CHAIN, GIZZ GALLUS GALLUS (CHICKEN). MAITA T., ONISHI H., YAJIMA E., M J. BIOCHEM. 102:133-145(1987). -!- FUNCTION: MUSCLE CONTRACTION. P10587; 01-JUL-1989 MYSG DOMAIN DOMĀIN NOD. MYOSIN; SEQUENCE OF 1-203 88032919 SUBMITTED (FEB-1989) YANAGISAWA M., HAMADA Y., KATSURAGAWA Y., IMAMURA M., MIKAWA T., 88118918 SEQUENCE FROM GALLIFORMES. EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE; WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE ARE CHICK MUSCLE PROTEIN; METHYLATION; N.A. 198:143-157 (1987) STANDARD; 11, CREATED)
13, LAST SEQUENCE UPDATE)
29, LAST ANNOTATION UPDATE)
N, GIZZARD SMOOTH MUSCLE. 848 1978 183 688 781 ö COILED COIL; THICK FILAMENT; ACTIN-BINDING; ALKYLATION; HEPTAD REPEAT PATTERN; EMBL/GENBANK/DDBJ DATA BANKS ACTIN-BINDING. ACTIN-BINDING. METHYLATION (TR BLOCKED.
GLOBULAR HEAD
RODLIKE TAIL (
ATP. FOR MYOSIN PRT; MATSUDA G.; 1978 AA DOMAIN ARE SELECTIVELY N ATPASE ACTIVITY. D (S1). (S2 AND LMM DOMAINS).

(TRI-) (POTENTIAL) RESULT ACCORDANCE OF THE SOLUTION OF THE SOLUT 밁 S В S B S B STTT Matches Query Match Best Local Matches Query Match 3.2%; Best Local Similarity 23.1%; 01-NOV-1990 (REL. 01-NOV-1990 (REL. 01-NOV-1990 (REL. TROPOMYOSIN ALPHA MOD\_RES MOD\_RES CONFLICT SEQUENCE IEES-MILLER J.P., GOODWIN I.O., HELFMAN D.M.;

MOL. CELL. BIOL. 10:1729-1742(1990).

-I. FUNCTION: THE FUNCTION OF TROPOMYOSIN IN SMOOTH MUSCLE AND NON-MUSCLE CELLS IS NOT CLEAR.

MUSCLE CELLS IS NOT CLEAR.

-I. SUBUNIT: DIMER OF AN ALPHA AND A BETA CHAIN.

-I. DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQUENCE EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY.

-I. TISSUE SPECIFICITY: BRAIN.

-I. ALTERNATIVE PRODUCTS: THE TROPOMYOSIN ALPHA-TM GENE PRODUCES, BY ALTERNATIVE SPLICING, THE FOLLOWING PROTEINS: STRIATED MUSCLE TM, SMOOTH MUSCLE TM, BRAIN TMBR-1, TMBR-2, TMBR-3, FIBROBLAST TM-2, TM-3, TM-5A, AND TM-5B. TPMZ\_RAT P18344; EMBI; M34136; RŇTMBR3A. PIR; C34787; C34787. PROSITE; PS00326; TROPOMYOSIN. BRAIN; COILED COIL; REPEAT; AI SEQUENCE 245 AA; 28343 MW; ALPHA-TM.
RATTUS NORVEGICUS (RAT)
EUKARYOTA; METAZOA; CHO 1037 hesmiselevrlkkeeksrqelekikrklegessdlheqiaelqaqiaelkaqlakkeee 1096 1097 lqaalarledetsqknnalkkireleshisdlqedlesekaarnkaek-qkrdlseelea 1155 90205854 TISSUE=BRAIN; SEQUENCE FROM N.A. EUTHERIA; 308 366 VDKSAGQVARNTGLLESQL-SRHDQMLSVHDIRLAD 250 HEASSAVQHVNLLKE-WS-NSLEKKVSLLQNESVEKNKSIQSLHNQICSFEIEIERQKEM 31 lqreld-qerklretaeadvaslnrriqlveeeldraqerlatalqkleeaekaadeser 89 LRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNR-VTE-LES 36; Similarity 20; Conse RODENTIA. 706 716 127 1978 3.1%; larity 23.5%; Conservative Conservative 706 716 127 · 228762 b STANDARD; 16, CREATED)
16, LAST SEQUENCE UPDATE)
16, LAST ANNOTATION UPDATE)
CHAIN, BRAIN-3 (TMBR-3). CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; ALKYLATION (SH-1).
ALKYLATION (SH-2).
MISSING (IN REF. 3).
2 MW; 16146389 CN; Score 128; DB 7; Pred. No. 1.75e-03; 28; Mismatches 34 ALTERNATIVE SPLICING; w; 256960 CN; 44; Mismatches Score 135; DB 5; Pred. No. 2.14e-04; PRT; 245 AA 69; 34; Length 1978; Length 245 MULTIGENE FAMILY. Indels Indels



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RESULT
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MOL. CELL. BIOL. 10:1729-1742(1990).

-!- FUNCTION: THE FUNCTION OF TROPOMYOSIN IN SMOOTH MUSC
MUSCLE CELLS IS NOT CLEAR.

-!- SUBUNIT: DIMER OF AN ALPHA AND A BETA CHAIN.

-!- DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE.

-!- DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE.

-!- TISSUE SPECIFICITY: BRAIN.

-!- TISSUE SPECIFICITY: BRAIN. TPMY RAT P18343; 01-NOV-1990 01-NOV-1990 01-NOV-1990 EMBL; M34134; RNTMBR2A.
PIR; B34787; B34787.
PROSITE; PS00326; TROPOMYOSIN.
BRAIN; COILED COIL; REPEAT; AI
SEQUENCE 251 AA; 28704 MW; RATTUS NORVEGICUS (RAT) EUKARYOTA; METAZOA; CHO! TISSUE=BRAIN; SEQUENCE FROM N.A. EUTHERIA; TROPOMYOSIN ALPHA 376 376 318 31 90 90 ALTERNATIVE PRODUCTS: THE TROPOMYOSIN ALPHA-TM GENE PRODUCES, BY ALTERNATIVE SPLICING, THE FOLLOWING PROTEINS: STRIATED MUSCLE TM, SMOOTH MUSCLE TM, BRAIN TMBR-1, TMBR-2, TMBR-3, FIBROBLAST TM-2, TM-3, TM-5A, AND TM-5B. lqreld-qerklretaeadvaslnrriqlveeeldraqerlatalqkleeaekaadeser 89 NTGLLESQLSRHDQMLSVHDIRLAD NTGLLESQLSRHDQMLSVHDIRLAD gmkviesraqkdeekmeiqeiqlke 114
::||: :::::::|:| : gmkviesraqkdeekmeiqeiqlke 114
::||: :::::::|:|: LQRVIDSQAEKLKEL-DKEIRPF-RQNWEEADSMKSSVESLQNRVTELESVDKSAGQVAR Similarity 20; RODENTIA. (REL. (REL. (REL. (REL. (REL. 3.1%; larity 23.5%; Conservative STANDARD; STANDARD; 16, CREATED)
16, LAST SEQUENCE UPDATE)
16, LAST ANNOTATION UPDATE)
16, CHAIN, BRAIN-2 (TMBR-2). 29,05 CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; CREATED)
LAST SEQUENCE UF
LAST ANNOTATION Score 128; DB 7; Pred. No. 1.75e-03; 28; Mismatches 34 ALTERNATIVE SPLICING; PRT; 400 400 298473 ON UPDATE) 257 251 Ω Ş A A IN SMOOTH MUSCLE AND NON-34; Length 251; MULTIGENE Indels THE 3, FAMILY. SEQUENCE Gaps 375

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RESULT
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Best Local
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01-APR-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
- DEVELOPMENTAL STAGE: TRANSIENTLY EXPRESSED DURING PERINATAL SKELETAL MUSCLE DEVELOPMENT. IT IS FIRST DETECTED LATE IN FETAL LIFE, IS MAXIMALLY EXPRESSED AT THE END OF THE 1ST POSTNATAL WEEK, AND IS NOT FOUND IN THE ADULT. ALTHOUGH THEIR EXPRESSION TEMPORALLY OFFICARES.

- SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC AND CHARGED RESIDUES, WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE, ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: MUSCLE CONTRACTION.

-!- FUNCTION: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
-!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
-!- SUBUNITS (MLC) 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-!- EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (1AM)

-!- EACH MYOSIN HEAVY CHAIN CAN BE SPLIT FORTHER INTO 1 HEAVY MEROMYOSIN (1AMM). IT CAN LATTER BE SPLIT FORTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2)

-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYOSIN HEAVY CHAIN, PERINATAL RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
85030490
                                                                    TPMM TRICO
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; K02111; RNMYHC PIR; A02991; A02991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PERIASAMY M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYOSIN; MUSCLE PROTEIN; COILED COIL; THICK FILAMENT; ATP-BINDING; HEPTAD REPEAT PATTERN; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- THERE ARE 10 OR MORE MYOSIN HEAVY CHAIN GENES IN
                                                                                                                                         377
                                                                                                                                                                        157
                                                                                                                                                                                                         317
                                                                                                                                                                                                                                         101
                                                                                                                                                                                                                                                                            257
                                                                                                                                                                                                                                                                                              42 qnaslina-kkklendvsglqseveeviqrarnaeekakkaitdaammaeelkkeqdtsa 100 | :::: | | |::::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONSERVE
                                                                                                                                    TGLLESQLSRHDQMLSVHDIRLADMDLGFQVLETASYNGVLIWKIRDYKRRKQEA
                                                                                                                                                                                                                                                                           QHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKIL
                                                                                                                                                                                                         HLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQVARN
                                                                                                                                                                                                                                                                                                                                            h 3.1%;
Similarity 22.3%;
39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                               <1
257 AA;
(REL. 14, CREATED)
(REL. 14, LAST SEQUENCE UPDATE)
(REL. 14, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WIECZOREK D.F., NADAL-GINARD 259:13573-13578(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNMYHC.
                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                               257
29843 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                          Score 131; DB 5;
Pred. No. 7.18e-04;
45; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                               LIGHT MEROMYOSIN (LMM).
; 288053 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKELETAL
                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                              Mismatches 83;
                                                                    284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₿.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                            Length 257;
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIN-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAT
                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                         431
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                           316
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TROPOMYOSIN, MUSCLE.
TRICHOSTRONGYLUS COLUBRIFORMIS.
CUKARYOTA; METAZOA; ACOELEMATES; NEMATODA; SECERNENTEA; STRONGYLIDA. FRENKEL M.J., SAVIN K.W., BAKKER R.E., WARD C.W.; MOL. BIOCHEM. PARASITOL. 37:191-200(1989). WARD O'DONNELL I.J., DINEEN J.K., WAGLAND B., LETHO S., WERKMEISTER J.A., 89339870 SEQUENCE FROM N.A. 90114326 PARTIAL SEQUENCE.

INT. J. PARASITOL. 19:327-335(1989).

-I- FUNCTION: TROPOMYOSIN, IN ASSOCIATION WITH THE TROPONIN COMPLEX, PLAYS A CENTRAL ROLE IN THE CALCIUM DEPENDENT REGULATION OF STRIATED MUSCLE CONTRACTION.

-I- SUBUNIT: HOMODIMER.
-I- DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQUENCE EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY.

-I- DEVELOPMENTAL STAGE: PRESENT IN L3 (THIRD STAGE), 14 AND ADULT

EMBL; J04669; TCTROP.

HSSP; P07751; 2SPC.

PROSITE; PS00325; COFILIN TROPOMYOSIN.

PROSITE; PS00326; TROPOMYŌSIN.

MUSCLE PROTEIN; COILED COIL; REPEAT.

CONFLICT 277 277 T -> R (IN REF. 2).

SEQUENCE 284 AA; 33050 MW; 355363 CN;

В Query Match Best Local Matches 287 / Match 3.1%; Local Similarity 20.5%; les 25; Conservative 85 vaalnrrmtlleeeleraeerlkiatekleeathnvd-eservrkv-mengsfqde-era 141 IQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEA 346 49; Mismatches 42; Score 131; DB 7; Pred. No. 7.18e-04; Pred. Length 284; Indels 6. Gaps 6

S В S 142 347 ntieaqlkeaq-mlae-ea-drkydevarklamveadleraeeraeagenkiveleeelr 198 DSMKSSVESIQNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLGFQ 406

밁 S 407 VL 199 vv 408 200

Search completed: Tue Mar 19 09:51:46 1996 Job time: 35 secs.



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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, Distribution rights by IntelliGenetics, Inc. U.K.

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Tue Mar 19 09:55:10 1996; MasPar time 1.86 Seconds 190.366 Million cell updates/sec

>US-08-404-852-3 (1-49) from (US08404832.pep

Description: Perfect Score Sequence: Score: DKYKCEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTACQESIVK

49

Scoring table: PAM 150 Gap 11

Searched: 62355 seqs, 7230759 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq20
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12

Statistics: Mean 22.842; Variance 90.056; scale 0.254

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	BB	ID	Description	Pred. No.
1	107	28.4	475	$\omega$	R15148	Ro/SSA autoantigen.	1.08e-02
N	83	22.0	69	11	R60623		1.49e+00
ω	82		365	_	P91461	C3	1.82e+00
4	76	20.2	560	ა	R27535	myl protein.	5.90e+00
5	76	20.2	797	G	R27533	myl/RAR-alpha fusion.	5.90e+00
0	74	19.6	165	N	R10533	Prod. of pMG4B12 used	8.69e+00
7	73	19.4		11	R60622	Pseudorabies virus ea	1.05e+01
æ	73	19.4		1	R60621	Pseudorabies virus ea	1.05e+01
9	72	19.1		12	R66033	Human ARD 1.	1.28e+01
10	71	18.8	574	12	R66034	Rat ARD 1.	1.54e+01
11	69	18.3		12	R63059	Rat PLA2 type I.	2.26e+01
12	69	18.3	146	12	R63052	HPLA2-8.	2.26e+01
13	69	18.3	185	10	R53530	Partial Thyroid hormo	2.26e+01
14	69	18.3	555	_	R05434	Sequence for lucifera	2.26e+01
15	69	18.3	555	N	R11108	Luciferase deduced fr	2.26e+01
16	68	18.0	118	_	P90076	Phospholipase A2-type	2.72e+01
17	67	17.8	104	0	R30630	Polypeptide coded by	3.28e+01
18	67	17.8	104	0	R30631	Polypeptide coded by	3.28e+01
19	67	17.8	2783	G	R23963	AFP-1 (Ala 2460 Val).	3.28e+01
20	67	17.8	2783	G	R23962	AFP-1.	3.28e+01

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. 61	61	61	61	5	61	61	62	62	62	62	62	62	62	62	62	62	63	63	64	64	64	64	65	66
16.2	16.2	16.2	16.2	16.2	16.2	16.2	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.7	16.7	17.0	17.0		17.0	17.2	17.5
		718		622								154				103 1		2458			77			208 1
	12				12 1		8					2							7					_
P91672	R66391	R05936	R68743	P91632	R68840	R60624	R44735	R23970	R07447	R60536	R05596	P82174	P50461	R53348	R12113	R70984	R07640	R04031	R39206	R10311	R34939	R14310	R69821	R60055
Primary amino acid se	Human SREBP-2.	Secreted GPIIIa subun	BCL-6 zinc finger pro	Rhoptry membrane anti	Plasmodium falciparum	ŧυ	apo-E lipoprotein rec	MPLV env protein with	Human laminin B1 chai	Mouse osteoblast-spec	Somatomedin carrier p	encoded	Sequence of the antig	Chicken (egg white) l	Lysozyme substrate fo	Component B protein.	Deduced protein seque	Full length T4 encode	Sequence of a peptide	Ovary tissue transcri	pZ70 polypeptide.	Tomato metallocarboxy	OMTKY3 (6-56) (A15R-T17	Dirofilaria immitis p
9.91e+01		9.91e+01	9.91e+01	9.91e+01	9.91e+01	9.91e+01	8.27e+01	8.27e+01	8.27e+01	8.27e+01	8.27e+01	8.27e+01	8.27e+01	8.27e+01	8.27e+01	8.27e+01	6.89e+01	6.89e+01	5.73e+01	5.73e+01	5.73e+01	5.73e+01	4.77e+01	3.96e+01

#### ALIGNMENTS

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RESULT
AC RIA
AC
                                                                                                                                                                                                                                                                   DNA encoding an Ro-SSA autoantigen - useful for diagnosing auto-immune disorders or presence of auto-antibodies bisclosure; Fig 2; 41pp; English.

A cDNA library (from human thymus mRNA) in lambda gtl1 was screened with serum from a patient having systemic lupus erythematosus. Two clones were reactive with sera (from a panel of lupus patients) which contd. autoantibodies against 52 kD protein.
                                                                                     Both the cDNA and the protein expressed from it, or portions of it are useful as diagnostic agents in the identification of patients having autoantibodies and in the identification and analysis of the structural and functional properties of the autoantigen and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens. W09117171-A.
    Sequence
                                          application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; Q14798.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Frank MB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-MAY-1991; U03139.
07-MAY-1990; US-520270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Autoantibody; autoantigen; SLE; systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ro/SSA autoantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R15148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R15148 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-NOV-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-FEB-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (OKLA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    k MB, Itoh K;
91-353712/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OKLAHOMA MED
B, Itoh K;
         A
A
                                                   immunotherapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RES
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                                               regimens.
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Query Match Best Local Similarity 28.4%; Score Pred. 107; DB 3; No. 1.08e-02; Length

1.54 100 mail: 13 

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Listing for Mary Hale Tue Mar 19 12:36:57 3 Ž. 1996

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Matches

12;

Conservative

13;

Mismatches

19;

**;** 

Gaps

o;

48 59 Indels

16 cpicldpfvepvsiecghsfcqecisqvgkgggsvcpvcrqrfl 5 CEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTACQESIV

/note= "cysteine: finger motif" US5352596-A. acid sequence specific to the LLT gene in the opposite orientation. Thus delection in the EPO gene other than the first 200 bp of EPO will automatically delecte some of the DNA sequences encoding the LLT. EPO is nonessential for replication, LLT (large latency transcript) is the only gene expressed during PRV latency, and the IE180 gene is absolutely necessary for PRV replication. However there are 2 copies of IE180 in the genome. It is expected that PRV lacking one of the IE180 copies is viable. Deletions in the non-overlapping regions of these 3 genes will generate single deletion routants, while deletions in overlapping regions LT 2 R60623 latency transcript gene
Disclosure; Column 45-47; 43pp; English.

R60622-24 show cysteine-rich zinc finger domains that is conserved among herpesviruses. This peptide is the homologous region from the Herpes simplex virus 1. This is the most important domain of the EPO gene. The DNA encoding this cysteine-rich domain (see Q73501) also encodes an amino control of the cysteine-rich domain (see Q73501) also encodes an amino control of the cysteine-rich domain (see Q73501) also encodes an amino control of the cysteine-rich domain (see Q73501) also encodes an amino control of the cysteine-rich domain (see Q73501) also encodes an amino cysteine-rich domain cysteine-rich domain cysteine-rich domain cysteine-rich domain cysteine-rich domain cysteine-rich d 11-SEP-1992; US-945283. (USDA) US SEC OF AGRIC. Cheung AK, Wesley RD; WPI; 94-316187/39. Pseudorabies virus; PRV; LLV; large latency transcript; attenuated virus; vaccine; early protein 0; EPO; HSV-1 ICPO; New pseudorables virus mutants for use in vaccine - having a deletion and/or insertion in the early protein O gene or large Misc difference 44 Misc difference 27 Misc\_difference 9 Misc\_difference Herpes simplex virus ICPO Pseudorabies virus; PRV; I Misc\_difference 41 Misc difference 30 protecting animals; deletion mutants; swine; cysteine-rich; 11-SEP-1992; 945283. 11-SEP-1992; US-9452 04-OCT-1994. /note= "cysteine finger motif" finger motif" /note= "cysteine finger motif" /note= "cysteine residue finger motif" Herpes simplex virus 1. /note= "cysteine residue finger motif\* /note= "cysteine residue .5-MAY-1995 (first entry) finger motif. standard; 9 Location/Qualifiers residue residue Protein; residue O protein domain homologous to part of EPO. LIV; large latency transcript; that that that that that that is 69 B st 18 18 15 18 part part part part part part of the ٥f of, of, of of the the the the the zinc zinc zinc amino

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Listing for Mary Hale

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RESULT 3
ID 991461;
AC P91461;
DT 10-MARDT 09-JANDE RPC-1 c
KW Regulat
KW human 1
OS Homo sa
PN W089076
PD 24-RUGPF 10-FEBPR 11-FEBPR 11-FEBPR 11-FEBPR WPI; 89
PT Cantor
DR WPI; 89
PT retrovi
PS Claim 2
CC DYNAN
CC Lymphom
CC positic
CC See alf
SQ Sequenc RESULT
ID R.
AC R.
DT 0
DE m
KW R δ 밁 밁 888888 δ Query Match Best Local S Matches Query Match Best Local Claim 20; fig 2; 58pp; English.

cDNA was prepd. from L cells (fibroblast tumour) and 2PK3 (B cell lymphoma). Host was pref. E. coli NRRL B-18297. Cysteine residues at positions 15, 18, 35, 38, 55, 58, 115 and 118, and histidine residues positions 124 and 127 may be involved in metal finger formation. Positions are given from the methionine (a.a.13 in the sequence give See also N90702. my1 protein.
Retinoic acid receptor;
APL; translocation; chro 10-FEB-1989; U00550. 11-FEB-1988; US-194758. (DANA) Dana-Farber Cancer Institute. Cantor HI, Patarca R, Freeman GJ; WPI; 89-263719/36. will generate double deletion mutants. The invention is concerned with the construction of attenuated viruses which have a reduced ability to reactivate from latency. This can be achieved by functionally disabling the expression of the EPO gene, or by disrupting the synthesis of the LTT, or both (See also Q73500-1 and R60620-24) R27535; 09-MAR-1993 Regulatory protein T lymphocyte-1 gene and corresp. protein - increa gene expression of interleukin-2 receptor and of human lymphotrophic R27535 24-AUG-1989 WO8907652-A. human lymphotrophic retroviruses; metal fingers. Rpt-1 clone cDNA insert.
Regulatory protein T lymphocyte-1; IL-2 receptor; 09-JAN-1990 Sequence 0-MAR-1993 27 20 24 G cmhrfcipcmktwmqlrnt-cplcnaklv 51 CEKCHLVLCSPKQTECGHRFCESCMA CGHRFCESCMAALLSSSSPKCTACQESIV standard; standard; Similarity Similarity 9; 69 365 21.8%; larity 34.6%; Conservative 22.0%; larity 34.5%; Conservative (first entry) (revised) Ŗ, Ā Protein; peptide; entry) RAR-alpha; omosome 17; 560 365 Score 83; Pred. No. 5; Misma Score Pred. 6; A B 30 Mismatches Mismatches 82; No. myl; acute chromosome 48 DB 11; 1 1.49e+00; DB 1; L 1.82e+00; 13; 11; promyelocytic leukemia;
15; PCR; primer; Length Length Indels Indels protein - increase 365; 69 0 1; Gaps Gaps given) 0, at 1

> The sequence given represents the amino acid sequence of one variation of the myl protein. The gene encoding this protein is disrupted in a translocation of a portion of the long arm of chromosome 17 onto the long arm of chromosome 15 [t(15,17)(q21,q11-22)]. This causes a fusion between retinoic acid receptor (RAR)-alpha and myl which is characteristic of acute promyelocytic leukemia (APL). The breakpoint region has been cloned and it has been shown that DNA rearrangements are clustered in the region of the first intron of RAR-alpha. This sequence was isolated by polymerase chain reaction (PCR). The primers N-PSDB; Q29354.
> Marker for acute promyelocytic leukaemia and comprising nucleic acid and encoded abnormal 01-OCT-1992. 23-MAR-1992; U02320. 22-MAR-1991; US-673838. 22-MAR-1991; US-675084. ₩. Dmitrovsky E, Warrell RP; used for amplification of this sequence can also be used to amplify the translocated region. Sequence 560 AA; receptor-alpha receptor Disclosure; Page 48-51; 84pp; WO9216660-A. Synthetic (SLOK ) SLOAN [t(15;17)(q21;q11-22)]; breakpoint; closure; Page 48-51; 84pp; English. sequence given represents the amino 92-349240/42. KETTERING Evans RM, Frankel INST CANCER. kel S, Kazizuka polymerase chain reaction. ۶ other neoplasias retinoic acid Miller WH; tusion

S В Matches Query Match Best Local 56 rcqqcqaeakc-pkllpclhtlcsgclea :1: 1: | | | | | | ; | ; | 4 KCEKCHL-VLCSPKQTECGHRFCESCMAA Similarity 10; Conservative 20 34 .5% Score Pred. 6; Mismatches 76; 83 Ω 5 DB 5; I 5.90e+00; Length Indels 560; 2; Gaps 2

myl/RAR-alpha 09-MAR-1993 R27533

(first

fusion.

standard;

Protein; entry)

797

A

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WPI; 92-349240/42.

N-PSDB; Q29334.

Marker for acute promyelocytic leukaemia and other neoplasias comprising nucleic acid and encoded abnormal retinoic acid receptor-alpha receptor
                                                                                                                                                                                     Retinoic acid receptor; RAR-alpha; myl; acute promyelocytic leukemia; APL; translocation; chromosome 17; chromosome 15; PCR; primer; [t(15,17) (q21;q11-22)]; breakpoint; polymerase chain reaction.
                                                                                                                                   01-OCT-1992.
23-MAR-1992; U02320
                                                                           22-MAR-1991; US-673838.
22-MAR-1991; US-675084.
(SLOK) SLOAN KETTERING
DMITTOVSKY E, EVANS RM,
                                                                   Warrell RÞ;
                                                                                                                                                             WO9216660-A.
                                                                               Frankel S,
                                                                                             INST CANCER.
                                                                              Kazizuka A, Miller
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chromosome

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Tue Mar 19 12:36:57 1996

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FREE COLD PRINTS OF PRINTS б 밁 %22222222222223 Best Matches Query Nictiana tabacum "Petit Havana" SR1. EP-412006-A. 4B12, obtd. from Prof. Goldberg of UCLA, into pGEMI, to produce pMG4B12. The clone was found to be stigma-style specific in Northern analysis. A probe from the clone was used to isolate the corresp. genomic sequence which is specifically expressed in style-stigma tissues of the female organ of tobacco. The corresp. clone, pSTG4B12, contains STMG4B12, an "STMG-type" gene. This and other similar genes can be used to produce new hybrid plants or seeds having a combination of desirable traits, and showing hybrid vigour. A female-sterile, male-fertile plant can be produced which Disclosure; Fig 4; 84pp; English.

The sequence given shows a fusion between retinoic acid receptor (RAR)-alpha and myl which is caused to a translocation of a portion of leukemia (APL). This is caused by a translocation of a portion of the long arm of chromosome 17 onto the long arm of chromosome 15 [t(15;17)(q21;q11-22)]. The breakpoint region has been cloned and it has been shown that DNA rearrangements eclustered in the region of the first intron of RAR-alpha. This sequence was isolated by polymerase chain reaction (PCR) using primers which correspond to sequences both 5' and 3' to the breakpoint region. foreign DNA encoding prod. which disrupts and/or development of plant.
Disclosure, Fig 2B; English.
The clone was produced by subcloning a sty T 6 R10533 standard; Protein; favours cross-pollination. See also R10531-35. Modified plant with transformed nuclear genome - obtd. by using foreign DNA encoding prod. which disrupts metabolism, functioning Van Montagu De (PLAN-) 04-AUG-1989; 06-FEB-1991. Prod. of pMG4B12 used to isolate style-stigma specific gene STG4B12 R10533 2-APR-1991 Local Greef W, Match 4 KCEKCHL-VLCSPKQTECGHRFCESCMAA 31 91-038878/06. -1989; EP-402224. -1990; EP-402196. ) PLANT GENETIC SY Q10376. 10; Similarity 797 AA; Van Emmelo J, (first entry) Conservative 20.2%; SYST. 165 De Oliveira Score Pred. 6; M A Mismatches 76; DB 5; No. 5.90e+00 83 a style-stigma specific DE, De 11; Souza Length Indels 797; 2; cDNA, Gaps

2:

Se 5, 1 

(a)

Query Match Best Local

Local Similarity

Conservative

Mismatches

Indels

2:

Gaps

2;

19.6%;

Score Pred.

74; No.

DB 2; Lemy . 8.69e+00;

Length 165;

Matches

1

Listing for Mary Hale

Tue Mar 19 12:36:57 1996

Page 50

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PT latency transcript gene
PS Disclosure; Column 45-46; 43pp; English.

CC R60622-24 show cysteine-rich zinc finger domains that is conserved among CC herpesviruses. This is the most important domain of the EPO gene. The DNA CC encoding this cysteine-rich domain (see Q73501) also encodes an amino CC acid sequence specific to the LIT gene in the opposite orientation. Thus CC deletion in the EPO gene of the DNA sequences encoding the LIT. EPO is connessential for replication, LIT (large latency transcript) is the only CC gene expressed during PRV latency, and the IE180 gene is absolutely CC necessary for PRV replication. However there are 2 copies of IE180 in the CC viable. Deletions in the non-overlapping regions of these 3 genes will generate single deletion routants, while deletions in overlapping regions will generate double deletion mutants. The invention is concerned with the construction of attenuated viruses which have a reduced ability to reactivate from latency. This can be achieved by functionally disabling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudorabies virus early polypeptide 0 homologous protein domain. Pseudorabies virus; PRV; LLV; large latency transcript; attenuated virus; vaccine; early protein 0; EPO; HSV-1 ICPO; protecting animals; deletion mutants; swine; cysteine-rich;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New pseudorables virus mutants for use in vaccine - having a deletion and/or insertion in the early protein O gene or large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-SEP-1992; 945283.
11-SEP-1992; US-945283.
(USDA) US SEC OF AGRIC.
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finger motif"
US5352596-A.
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finger motif"
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Page 51

б 밁 8888 PT deletion and/or insertion in the early protein O gene or large
PT latency transcript gene
PT latency transcript gene
PS Disclosure; Column 39-44; 43pp; English.
CC R60521 shows the early polypeptide O (EPO) encoded by Q73501. The
CC most important of the EPO gene is likely to be the cysteine-rich zinc
CC finger domain from amino acids 40 to 100, since this region is conserved
CC among other herpesviruses (eg. see R60622-24). The DNA encoding this
CC cysteine-rich domain also encodes an amino acid sequence specific to the
CC LIT gene in the opposite orientation. Thus deletion in the EPO gene
CC other than the first 200 bp of EPO will automatically delete some of the
CC CNA sequences encoding the LLT. EPO is nonessential for replication, LLT
CC (large latency transcript) is the only gene expressed during PRV latency,
CC and the IE180 gene is absolutely necessary for PRV replication. However
CC there are 2 copies of IE180 in the genome. It is expected that PRV
C1 lacking one of the IE180 copies is viable. Deletions in the
CC non-overlapping regions of these 3 genes will generate single deletion
CC routants, while deletions in overlapping regions will generate double Matches Query Match Best Local Pseudorabies virus early polypeptide 0.
Pseudorabies virus; PRV; LLV; large latency transcript; attenuated virus; vaccine; early protein 0; EPO; HSV-1 Cheung AK, Wesley RD; WPI; 94-316187/39. 11-SEP-1992; 945283. 11-SEP-1992; US-945283. (USDA) US SEC OF AGRIC. R60621 standard; R60621; the expression of LLT, or both. (See Sequence 67 AA; New pseudorabies virus mutants for use in vaccine - having N-PSDB; Q73501. Domain
/label= zinc finger motif
/note= "cysteine rich" Domain protecting animals; deletion mutants; note= "cysteine rich seudorabies virus. 5 6 cpicldvaateaqtlpcmhkfcldciqrwtltstacplckarvtsil 52 CEKCHLVLCSPKQT-ECGHRFCESCMA---ALLSSSSPKCTACQESIV 48 α Similarity Conservative 40.. 46..49 Location/Qualifiers Protein; 410 also the 19.4%; EP0 gene, to Q73500-1 zinc finger domain" Score Pred. 7; M B or by disrupting and R60620-24) Mismatches No. 1.05e+0 swine 20; Length the synthesis of the Indels ICPO; ø ψ Gaps 2

Listing for Mary Ha 2 Tu 

888888

Sequence

410

AA,

attenuated viruses which have a reduced ability to reactivate from latency. This can be achieved by functionally disabling the expression the EPO gene, or by disrupting the synthesis of the LLT, or both. (See also Q73500-1 and R60620-24)

of

deletion mutants. The invention is concerned with the construction of

В

46 cpicldvaateaqtlpcmhkfcldciqrwtltstacplcnarvtsil

Matches Query Match Best Local :

Local Similarity nes 17; Conser

19.4%; larity 36.2%; Conservative

Score 73; DB 11; Pred. No. 1.05e+01; 7; Mismatches 20

20;

Indels 92

Ψ

Gaps

2

Length 410;

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Page 52

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Query Match
Best Local Similarity
                                                                                    to the amino terminus of ARF proteins are not required for toxin activation. cDNA was isolated from a human HL-60 lambda library screened with ARF 2B cDNA and a mixture of oligos denoted XARFC. Clone no. 76 was positive with the ARF 2B cDNA and negative with oligos specific for ARFs 1-6. The insert was sequenced. The insert (2D7-172) encoding insert (2D7-172) encoding an ARF domain of 172 AAs. Oligo JIR was used to screen a human fetal brain cDNA lambda ZAP library. Clones were found contg. nucleotides 7-1826 and 726-3225 of 079326. In this sequence, about 1200 nts preceded the ARF region without a stop codon in the same ORF. To further characterise the 5' terminus of this cDNA, 5'-RACE carried out with the poly A+ RNA from IMR-32 human
                                                                                                                                                                                                                                                                                                                      GTP-binding protein ARD1 with ADP-ribosylation factor domain—
useful as biochemical and diagnostic reagent
Claim 5; Page 24-27; S2pg; English.

The novel ARD 1 protein includes an 18 kDa region that
exhibits significant homology to known ADP-ribosylation factors
(ARFs) but lacks a 15 AA domain previously thought necessary for ARF
stimulation. The 18 kDA region is called the functional domain and
it is at the carboxy terminus. It is called ARD 1 for ARF domain. A
recombinant truncated species contg. only the ARF domain following
expression activated cholera toxin ADP-ribosyltransferase in a GTP-
dependent manner, consistent with the conclusion that 15 AA adjacent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; Q79326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mishima K, Moss J
WPI; 94-341862/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 9
R66033 standard; Protein; 574
                                                         neuroblastoma cells.
Sequence 574 AA;
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19-APR-1993; US-049473.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moss J, Nightingale
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor; ARF domain; ARD 1.
 19.1%;
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 Score
Pred.
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No.
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 DB 12;
1.28e+01;
                 Length 574;
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Matches

9

Conservative

6;

Mismatches

11;

Indels

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Gaps

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PER COLOR OF S 밁 Query Match Best Local S Matches 15-AUG-1995 (first entry)
Rat PLA2 type I.
RPLA2; RPLA2-8; RPLA2-10; phospholipase A2; PLA2.
Homo sapiens.
W09502328-A. 19-APR-1993; US-049473. (USSH) US DEPT HEALTH & HUMAN SE Mishima K, Moss J, Nightingale WPI; 94-341862/42. R63059, R63059 standard; Protein; 124 Sequence N-PSDB; Q79327. 16-APR-1993; Rattus rattus. ADP-ribosylation factor; ARF; Rat ARD 1 05-JUN-1995 (first entry) R66034 R66034 standard; 51 46 20 Local Similarity 15 cghtvchdclsrlalhgrairc PKQTECGHRFCESCMAAL-LSSSSPKC CGHRFCESCMAAL-LSSSSPKC prlllcghtvchdcltrlplhgrairc 574 AA; Conservative Protein; 18.8%; & HUMAN SERVICES. 574 Score Pred. 5; M 40 72 Ą ARD B e 71; DB 12; Len 1. No. 1.54e+01; 1. No. 1.54e+01; 40 72 Ļ. probe. Length 574; Indels 1; Gaps

RESULT
ID R
AC R
DT 1.
DE R
KW R
OS H
PN W
PD 2 S 밁 PT GTP-binding protein ARD1 with ADP-ribosylation factor domain - GTP-binding protein and diagnostic reagent research as biochemical and diagnostic reagent stample; Table I, Page 11-12; 52pp; English.

CC A novel ARD 1 protein includes an 18 kDa region that can be received as a significant homology to known ADP-ribosylation factors (ARFs) and is called ARD 1 for ARF domain. Following transfection of CC (ARFs) and is called ARD 1 for ARF domain. Following transfection of CC reverse transcribed, PCR amplified human sequences into competent DH5 creation of 574 AAs with an ARF related domain at the carboxyl carminus (see Q79326/R66033). Clones corresp. to rat ARD 1 were isolated. A rat brain Lambda ZAPII library was screened with oligo CR ASSCR. It yielded clone 2a contg. an insert that corresp. to nts CC 61-1973 of human ARD 1. 079327 and R6034 give the cDNA and deduced CC AA sequence of rat ARD1 which corresp. to the CDNA and deduced CC Nt and deduced AA sequences of ARD 1 coding regions from rat and CC human are 92t and 98t identical, respectively, without any gaps. 26-JAN-1995 ۲

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Best Local
                         Disclosure; Page 67-76; 160pp; English.

A human PLA2-encoding cDNA (Q81138) expressing HPLA2-10, was a human PLA2-encoding cDNA (Q81138) expressing HPLA2-10, was a lisolated from human brain RNA by RACE-PCR. 2 Rat PIA2 cDNAs, designated RPLA2-8 (Q81136) and RPLA2-10 (Q81137), were isolated frow rat brain and heart cDNA libraries, respectively. A partial human genomic counterpart to RPLA2-8, HPLA2-8 (Q81139), was also obtained. RPLA2-8 and HPLA2-8 have been designated type III PLA2, and RPLA2-10
                                                                                                                                      N-PSDB; Q81139.

N-PSDB; Q81139.

Novel type III and IV low mol. wt. phospholipase A2 enzymes from humans and rats, also nucleic acid sequences useful, e. for recombinant prodn. of enzymes, research into Batten's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig. 27; 160pp; English.
Rat cDNAs (Q81136-37) encoding 2 novel PLA2s, RPAL2-8 (R63044) and RPLA2-10 (R63045), were isolated from brain and heart libraries, respectively. RPAL2-8 and RPLA2-10 were characterized as novel type III and IV PLA2s on the basis of their cysteine content compared with RPLA2 types I (R63059) and II (R63059). Sequence 124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel type III and IV low mol. wt. phospholipase A2 enzymes from humans and rats, also nucleic acid sequences useful, e for recombinant prodh. of enzymes, research into Batten's
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26-UUL-1993; US-097354.
(INCY-) INCYTE PHARM INC.
(INDV ) UNIV INDIANA FOUND.
Seilhamer JJ, Tischfield J
                                                                                                                                                                                                                                                                                            15-JUL-1994; U07926.
15-JUL-1993; US-091941.
26-JUL-1993; US-097354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              R63052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 12
R63052 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seilhamer JJ, Ti.
WPI; 95-067096/09
and HPLA2-10 as type IV. Sequence 146 AA;
                                                                                                                                                                                                                             Seilhamer JJ, Tiso
WPI; 95-067096/09.
                                                                                                                                                                                                                                                                                                                                                                                           HPLA2-8; phospholipase A2; PLA2; Batten dise neuronal ceroid lipfuscinosis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease, etc.
                                                                                                                                                                                                                                                                                                                                            26-JAN-1995.
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L5-JUL-1994; U07926
                                                                                                                                                                                                                                                          (INCY-) INCYTE PHARM INC. (INDV ) UNIV INDIANA FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                           5-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 ykcsg-nvitcsdknndcesficn-c 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 YKCEKCHLVLCSPKQTECGHRFCESC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                            Tischfield JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein; 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.3%;
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                              Batten disease;
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2.26e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                              from
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1

Query Match Best Local

Similarity 9

18.3%; larity 34.6%; Conservative

Score Pred. 6; N

69;

DB 12; . 2.26e+01; -has 9;

Length 146 Indels

Mismatches

2;

Gaps

2

#### Tue Mar 19 12:36:57

1996

Page 55

1

RESULT 13
ID R53500;
AC R55300;
AC R55300;
DT O3-FEBDE PARTIAL
IXW NUCLEAR
ON HOMO SAI
FH Key
FT Commain
FT /label=
FT Misc di
FT /note=
FT Misc di
FT /no 5 В Partial Thyroid hormone receptor-interacting protein - JL2. nuclear thyroid hormone interacting proteins; TR; JL1; JL2; LIM domain; consensus motif; lin-1; is1-j; mcc-3; transcriptional coactivator; treatment; diagnosis; thyroid related disorders; modulation; thyroid hormone receptor; nuclear hormone receptor; fusion proteins; isolation. /note= "consensus Cys" Misc\_difference 77 /label= LIM\_domain\_II
Misc\_difference 30 Misc\_difference Misc\_difference 53 /note= "consensus Cys" Misc\_difference 33 Homo sapiens. 03-FEB-1995 /label= LIM\_domain\_I Domain 90..151 97 e= "consensus ( \_difference 50 ykcsg-nvitcsdknndcesficn-c 120 YKCEKCHLVLCSPKQTECGHRFCESC 28 standard; "consensus Cys" "consensus His" (first entry) 30..81 Location/Qualifiers protein; 185 Сув\* A

Misc difference 151
Misc difference 151
- "consensus Cys" Lee JW, Moore DD; WPI; 94-199808/24. 30-OCT-1992; US-969136. (GEHO ) GEN HOSPITAL CORP 29-OCT-1993; U10443. 30-OCT-1992; US-969136 11-MAY-1994

밁

39 ceakegecidtrcatckrdilsdg

Matches

Local Similarity

Pred.

N

6 62

Mismatches

Indels

0

Gaps

0

/note= "consensus F Misc\_difference 78

His\*

/note= "consensus Cys" Misc\_difference 117

Misc difference 123
/note= "conserved"

Misc\_difference 120

\*consensus

His"

Misc difference 148
/note= "common"

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> Listing for Mary Hale ĮĮ.

> > Tue Mar 19 12:36:57 1996

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TRESULT
RESULT
ACCOMENTATION
A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the protein. TR-interacting proteins physically associate with thyroid hormone receptor. Nearly all the fusion associate with thyroid hormone receptor. Nearly all the fusion cDNAs showed very strong dependence on hormone activation. The proteins can be used in an in vivo trap system for the isolation of proteins which associate with any nuclear hormone receptor. The proteins and Abs may be used to treat or diagnose thyroid disorder and to modulate thyroid hormone receptor activity. (See also R33530-57 and Q63681-705.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nuclear hormone receptor interacting polypeptides, esp. thyroid hormone=interacting proteins (TRs) - for identifying proteins useful in treatment and diagnosis of thyroid related disorders by inoculating thyroid hormone receptor activity claim 10; Page 40-41; 105pp; English.

This sequence shows the complete amino acid sequence of JL2, a thyroid hormone (TR) interacting protein, that has 2 LIM (LIM = Lin-11, isl-1, mec-3 - putative transcription factors) domain consensus sequences containing conserved cysteine (or asparagine) and histidine residues. The sequence shows only the human portion
                                                                                                                                                                                    Recombinant luciferase, fragments from it, and gene coding for it -
the luciferase having increased stability and quantum yield.
Claim; Fig 1A-1D; 56pp; Japanese.
A recombinant vector wherein the luciferase-coding gene is connected
to the downstream portion of a promoter capable of expressing in a host
cell allows for the production of luciferase, having increased stability,
better quantum yield and light production conditions. Light of different
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R05434
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Kazami J, Nakamura H, Goto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cypridina hilgendorfii ('umihotaru').
WO9001542-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence for luciferase.
Luciferase; ss.
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ilarity 33.3%;
Conservative
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                                                                  Length 555;
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Ś 13 CSPKQTECGHRFCESCMAALLSSS 36

R11108 standard; Protein; 555 AA. R11108; 23-MAY-1991 (first entry)

Luciferase deduced from cDNA. luciferin; luminescence. Vargula hilgendorfii.

J03030678-A.

29-JUN-1989; 167689. 29-JUN-1989; JP-167689. (OHSA-) OHSAKA BIOSCIENCE WPI; 91-084343/12. <u>بر</u>

N-PSDB; Q10957.

DNA cpd. coding luciferase derived from Vargula hilgendorfii - by transfection of host cells and culturing.

Claim 1; Fig 3; 11pp; Japanese.

The cDNA encoding the protein is used to prepare vector pRSVVL which is used to transfect COS cells (ATCC CRL1650) for expression of luciferase. The enzyme is useful for assays in biomedical or environmental fields.

Sequence 555 AA;

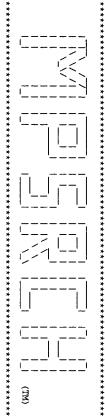
Query Match 18.3%; Best Local Similarity 33.3%; Matches 8; Conservative Score 69; DB 2; I Pred. No. 2.26e+01; 6; Mismatches 10 10; Length 555; Indels 0; Gaps

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1

S DЬ 13 CSPKQTECGHRFCESCMAALLSSS 36 39 ceakegecidtrcatckrdilsdg 62

Search completed: Tue Mar 19 09:55:19 1996 Job time : 9 secs.



Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tue Mar 19 09:54:27 1996;

MasPar time 3.63 Seconds 341.191 Million cell updates/sec

١ Tabular output not generated

Run on:

Listing for Mary Hale

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58

Description: Perfect Score: (1-49) from USO8404832.pep 377 1 DKYKCEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTACQESIVK >US-08-404-832-3

Sequence:

Scoring table: PAM 150 Gap 11

Searched: 82306 seqs, 25270970 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 8:unann5 9:unann6 10:unann7 11:unann8 12:unrev1 13:unrev2

7:unann4

Statistics: Mean 30.545; Variance 66.324; scale 0.461

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Score	Query Match	Length D	Ħ	ID	Description	Pred. No.
377	100.0	568 1	-	A55649	TNFR-associated prot	8.71e-52
120		77	<u> </u>	73	G finger-cont	.45e-
109	28.9			A54652	÷	
107	28.4			A37241	autoantigen Ro/	. 80
105	27.9			S44379	RAG-1 protein - rabb	
105	27.9			S42511	1 protein -	.54e-
102	27.1			S53400	3.3 protein -	
102	27.1			DDBY18	teir	4.24e-04
102	27.1			A33754	recombination-activa	4.24e-04
99	26.3			S34825	uvs2 protein - Neuro	
99	26.3			A43906	nuclear phosphoprote	1.16e-03
98	26.0			B33754	recombination-activa	
97	25.7			S55494	zinc	2.24e-03
94				S00530	antigen	
94	•			B42125	cysteine-rich surfac	
94	•			S28418	probable zinc-bindin	٠
94	•			A56095	HIP116 protein - hum	•
94				S49618	helicase-like transc	
94	•			S42509	l protein	•
90	•			S28290	thetical	2.18e-02
85				A44272	ന	•
85	•			S44866	R05D3.4 protein - Ca	1.06e-01
85	•			S31301	DNA repair protein R	1.06e-01
83	•			D48560	immediate-early prot	97e
83				S34203	heat shock protein 7	1.97e-01
83	•			S28712	heat shock protein 7	1.97e-01
83	•			A49656	estrogen-responsive	1.97e-01
83			ω	EDBE11	immediate-early prot	
82	•		س	S17880	posterior s	
82	•		-	A30891	latory	2.68e-01
82	•		Ö	S17983	gene posterior sex c	2.68e-01
	Score 377 129 1109 1109 1109 1109 99 99 99 99 99 99 99 99 99 99 99 99 9		Query Hardh Length 110.0 378 110.0 378 110.0 378 110.0 378 110.0 378 128.9 1863 228.9 1042 27.9 1042 27.1 128 27.1 1043 26.3 501 26.3 1043 25.7 477 24.9 1043 24.9 1049 24.9 1009 24.9 1009 24.9 1009 24.9 1009 25.5 658 22.0 598 22.0 598 22.0 598 22.0 598 22.0 598 22.0 775 21.8 3653	Match Length DB  100.0 568 11 378 11 378 1863 10 28.9 1863 10 27.9 1042 11 27.9 1042 11 27.1 259 9 27.1 1043 11 26.3 501 12 26.3 501 12 26.3 1043 11 25.7 477 9 24.9 498 12 24.9 498 12 24.9 1009 10 24.9 1009 10 24.9 11009 10 24.9 11009 10 24.9 11009 10 24.9 11009 10 24.9 11009 10 24.9 11009 10 24.9 11009 10 24.9 11009 10 24.9 1009 10 24.9 1009 10 24.9 1009 10 24.9 1009 10 24.9 1009 10 24.9 1009 10 24.9 1009 10 24.9 1009 10 24.9 1009 10 24.9 1009 10 25.5 658 834 10 27.5 1834 10 27.5 1834 10 27.5 598 7 27.0 598 7 27.0 598 7 27.0 598 7 27.0 630 17 27.1 8 365 13 21.8 365 13 21.8 365 13	Query Query Match Length DB ID 10.0 568 11 A4738 28.9 1863 10 A5462 28.4 475 2 A3724 27.9 1042 11 S4251 27.1 1259 9 S5340 27.1 1043 11 A3375 26.3 501 12 S4382 26.3 501 12 S4382 26.3 1043 11 B3375 25.7 477 9 S5549 26.9 1043 11 B3375 25.7 477 9 S5549 26.9 1043 11 S4251 24.9 1009 10 A5609 24.9 1009 10 S2981 24.9 1009 10 S4981 25.5 658 8 A4427 22.5 5834 10 S4486 22.0 598 7 S3420 22.0 598 7 S3420 22.0 598 7 S3420 22.0 630 10 A4962 22.0 630 10 A4962 22.0 598 7 S3420 22.1 630 10 A4962 22.1 630 10 A4962 22.1 630 10 A4963 21.8 365 11 A3089 21.8 365 11 A3089	Query Match Length DB ID    Description

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## Tue Mar 19 12:36:58 1996

A Comment

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81 79 79 78 78 78 76 76 76	
21.5 21.0 21.0 20.7 20.7 20.7 20.7 20.4 20.2 20.2 20.2 20.2 20.2 20.2	
713 208 1 670 1141 798 798 798 1548 1 324 324 324 560 659 802 802 802 1429	
13 9 6 6 11 11 11 11 11 11 11 11 11	
A35502 S38745 PS53414 PS53414 PS53419 H28193 A28193 A28193 A39523 A40044 TVMSBF S44386 S44386 S44386 S44380 S06434	
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#### ALIGNMENTS

Db 49 dkykcek           Oy 1 DKYKCEK	Query Match 100.0%; Best Local Similarity 100.0%; Matches 49; Conservative	53-91 SUMMARY	##note  KEYWORDS	##residues		#title	rs		##note	##cross-ref	##residnes 1-56	Haccession			#journal (	#authors !	REFERENCE		ALTERNATE_NAMES	i i
dkykcekchlvlcspkqtecghrfcescmaallsssspkctacqesivk 97 	100.0%; Score 377; DB 11; Length 568; larity 100.0%; Pred. No. 8.71e-52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	#region RING-finger motif #length 568  #molecular-weight 64490  #checksum 8660	##note incleotide sequence not given ps coiled coil	Cype mxwA 1-133,135-404,'G',406-568 ##label HUA	domain of CD40.	A novel RING finger protein interacts with the cytoplasmic	lu, H.M.; O'Rourke, K.; Boguski, M.S.; Dixit, V.M.	A55135	nucleotide sequence not given	##cross-references GB:U19260	Sypermana 1-568 ##label MOS	A55649	signating proteins for the tumor necrosis factor receptor family.	The Epstein-Barr virus transforming protein LMP1 engages	2ell (1995) 80:389-399	Mosialos, G.; Birkenbach, M.; Yalamanchili, R.; VanArsdale, T.: Ware. C.: Kieff R.	A33649; A33133 A55649	<pre>#formal_name Homo saptens #common_name man 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 05-Apr-1995</pre>	INFR-ASSOCIATEG PROTEIN LAFI - numan CD40-binding protein	A55649 #type complete

Listing for Mary Hale

Tue Mar 19 12:36:58 1996

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ACCESSIONS
REFERENCE
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O'Reilly, N.J.; Evan, G.I.; Rahman, D.; Pappin, D.J.;
Trowsdale, J.; Freemont, P.S.
#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:2112-2116
Identification and preliminary characterization of a protein motif related to the zinc finger.
#cross-references_MUID:93211912
                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors
                                                                               #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #accession
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##molecule type DNA; protein
##residues 1-377 ##label LOV
##residues 10-377 ##label LOV
##coss-references NCBIN:128010; NCBID:128011
##cross-references NCBIN:128016 from NCBI backbone
##note sequence extracted from NCBI backbone
##note #length 377 #molecular-weight 39145 #chec
##status preliminary; not compared with conceptual translation
##molecule_type mRNA
##residues 1-1863 ##label MIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 31.8%;
Similarity 34.8%;
16; Conservative
                                                                                                                                                                                              Miki, Y.; Swensen, J.; Shattuck-Eidens, D.; Futreal, P.A.; Harshman, K.; Tavtigian, S.; Liu, Q.; Cochran, C.; Bennett, L.M.; Ding, W.; Bell, R.; Rosenthal, J.; Hussey, C.; Tran, T.; McClure, M.; Frye, C.; Hattier, T.; Phelps, R.; Haugen-Strano, A.; Katcher, H.; Yakumo, K.; Gholami, Z.; Shaffer, D.; Stone, S.; Bayer, S.; Wray, C.; Bogden, R.; Shaffer, D.; Stone, S.; Bayer, S.; Wray, C.; Bogden, R.; Dayananth, P.; Ward, J.; Tonin, P.; Narod, S.; Bristow, P.K.; Norris, F.H.; Helvering, L.; Morrison, P.; Rosteck, P.; Lai, M.; Barrett, J.C.; Lewis, C.; Neuhausen, S.; Cannon-Albright, L.; Goldgar, D.; Wiseman, R.; Kamb, A.; Schlick, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A54652
A54652
                                                                            A54652
                                                                                                                         Skolnick, M.H.
Science (1994) 266:66-71
A strong candidate for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A54652 #type complete
breast/ovarian cancer seeptibility protein BRCA1 - human
#formal name Homo sapiens #common name man
15-oct-T994 #sequence_revision 15-oct-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A47380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A47380 #type complete
RING finger-containing DNA binding protein RING1 - human
#formal name Homo sapiens #common name man
21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A47380
                                                                                          susceptibility gene BRCA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-Dec-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-Nov-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 120; DB 11; Length 377; Pred. No. 8.45e-07; 11; Mismatches 18; Indels
                                                                                                                               the breast and ovarian cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #checksum 7895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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ACCESSIONS REFERENCE Ś В #gene GDB:BRCA1
#map position 17q12-q21
KEYWORDS zinc finger
SUMMARY #length 1863 GENETICS REFERENCE REFERENCE GENETICS ALTERNATE\_NAMES ORGANISM RESULT Query Match Best Local S Matches 1 #journal #title #journal #title #cross-references MUID:91086445 #accession A37241 ERENCE A37240

Fauthors Chan, E.K.L.; Hamel, J.C.; Buyon, J.P.; Tan, E.M.

# journal J. Clin. Invest. (1991) 87:68-76

# title Molecular definition and sequence motifs of the 52-kD

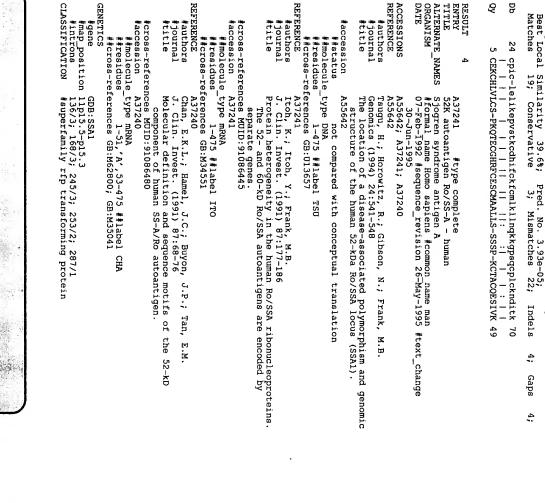
component of human SS-A/Ro autoantigen.

# cross-references MUID:91086480

# accession A37240 #accession #authors fauthors \*\*restdues 1-475 ##label ITO ##cross-references GB:M34551 NCE ##molecule\_type mENA ##residues 1-51,'A',53-475 ##label CHA ##cross-references GB:M62800; GB:M35041 ##cross-references GB:U14680 #molecule\_type mRNA ##molecule\_type DNA #status #residues 24 cpic-lelikepvstkcdhifckfcmlkllnqkkgpsqcplcknditk 70 5 CERCHLVLCS-PROTECGHRFCESCMAALLS-SSSP-KCTACQESIVK 49 residues 1-475 ##label TSU cross-references GB:U13657 h 28.9%; Similarity 39.6%; 19; Conservative Sjogren syndrome antigen A
#formal name Homo sapiens #common name man
07-Feb-1992 #sequence\_revision 26-May-1995 #text\_change A55642 A55642; A37241; A37240 A37241 #type complete 52K autoantigen Ro/SS-A - human A37241 A55642 30-Jun-1995 not compared with conceptual translation #molecular-weight 207755 #checksum Score 109; DB 10; I Pred. No. 3.93e-05; 3; Mismatches 22; Length 1863; Indels 4. 1680 Gaps

DATE RESULT ENTRY TITLE В RESULT ENTRY TITLE KEYWORDS SUMMARY δ S В ACCESSIONS REFERENCE SUMMARY REFERENCE DATE ORGANISM ACCESSIONS ORGANISM Matches Query Match Best Local : Matches Query Match Best Local #journal #title #accession #accession #authors #description #authors submission ##molecule type DNA
##residues 1-1000 "" 292 cqicehiladpvetsckhvfcricilrclkvmgsycpscq 331 ##status ##cross-references EMBL:M77666

# #length 1042 #molecular-weight 119006 #checksum Y Match 27.9%; Local Similarity 35.0%; 16 cpicldpfvepvsiecghsfcqecisqvgkgggsvcpvcrqrff 59 G 5 CEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTACQESIV 48 CEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTACQ h 28.4%; Similarity 27.3%; 12; Conservative genes. \$44379 Fuschiotti, P.; Harindranath, N.; Mage, R.G.; McCormack, W.T.; Dhanarajan, P.; Roux, K.H. submitted to the EMBL Data Library, December 1991 Recombination activating genes -1 and -2 of the rabbit: cloning and characterization of germline and expressed Fuschiotti, P.; Harindranath, N.; Mage, R.G.
W.T.; Dhanarajan, P.; Roux, K.H.
Mol. Immunol. (1993) 30:1021-1032
Recombination activating genes-1 and -2 of cloning and characterization of germline 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change S42511 #ty RAG-1 protein 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change RAG-1 DNA binding; nucleus; zinc finger #length 475 #molecular-weight 54169 #checksum #Iorma. S44379 #formal Conservative rormal name Oryctolagus cuniculus #common\_name domestic rabbit formal\_name Oryctolagus cuniculus #common\_name
 rabbit genes 13-Jan-1995 06-Jan-1995 1-1042 ##label FUS preliminary #type complete in - rabbit #type complete in - rabbit Score 105; DB 11; Length 1042; Pred. No. 1.54e-04; Score 107; DB 2; Pred. No. 7.80e-05; Mismatches 19; Indels Mismatches 19; Length 475; Indels of the rabbit: ine and express R.G.; McCormack, expressed ç **?** 7482 domestic 8825 Gaps Gaps



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S В SUMMARY Query Match 292 cqicehiladpvetsckhvfcricilrclkvmgsycpscq 331 ##cross-references EMBL:M77666 X #length 1042 #molecular-weight 118992 #checksum ##molecule\_type DNA ##residues Local Similarity 5 CEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTACQ 44 27.9%; larity 35.0%; Conservative 1-1042 ##label FUS Score 105; DB 11; Length 1042; Pred. No. 1.54e-04; 7; Mismatches 19; Indels 0 0; 8787 Gaps

0;

RESULT ENTRY REFERENCE ORGANISM TITLE ACCESSIONS #description morssimdus# #authors ##molecule\_type DNA
##residues 1-250 \*\*\* ##cross-references EMBL:U20618
# #length 259 #molecular-weight 29741 #checksum submitted to the EMBL Data Library, February 1995 The sequence of S. cerevisiae cosmid 8543. \$53400 #formal name Saccharomyces cerevisiae
05-May-1995 #sequence\_revision 01-Sep-1995 #text\_change \$53400 #type con 18543.3 protein -S53390 01-Sep-1995 1-259 ##label DUZ #type complete yeast (Saccharomyces cerevisiae)

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Ó DЬ Matches Query Match Local 3 YKCEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTACQ 44 h 27.1%; Similarity 40.5%; 17; Conservative Score 102; DB 9; Pred. No. 4.24e-04; 6; Mismatches 18 18; Length 259; Indels Gaps 1.

RESULT ALTERNATE NAMES ORGANISM REFERENCE ACCESSIONS #Journal Jones, J.S.; Weber, S.; Prakash, L.
#journal Nucleic Acids Res. (1988) 16:7119-7131

The Saccharomyces cerevisiae RADJ8 gene encodes a protein that contains potential zinc finger domains for nucleic acid binding and a putative nucleotide binding sequence.
#cross-references MUID:88303333
#accession S05802 00 DDBY18 #type complete
DDB repair protein RAD18 - yeast (Saccharomyces cerevisiae)
protein YCR066w
#formal name Saccharomyces cerevisiae
1-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 12-May-1995 \$05802; \$22263; \$19481; J\$0082

##cross-references EMBL:X12588 ##molecule\_type DNA 1-487 ##label JON

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EEYWORDS
FEATURE
28-48
51-65
190-210 ACCESSIONS REFERENCE RESULT ENTRY TITLE DATE S 밁 #map\_position CLASSIFICATION ORGANISM SUMMARY GENETICS REFERENCE REFERENCE REFERENCE Query Match 27.1%; Best Local Similarity 37.5%; #journal #title #journal #title #accession #authors Benit, P.; Chanet, R.; Fabre
Sor, F.
#journal Yeast (1992) 8:147-153
#title Sequence of the sup61-RAD18
Saccharomyces cerevisiae.
#cross-references MUID:92221691
#accession \$22263 #authors #cross-references MUID:89232745 #accession submission #authors fgene authors ##cross-references EMBL:S93798
NCE S19477
thore ##molecule\_type DNA ##residues 1-487 ##label CHA ##molecule\_type DNA #residues 1-487 ##label ANT ##cross-references EMBL:X59720 ##molecule\_type DNA 4 KCEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTAC 43 9 Antoine, G.; Benit, P.; Chanet, R.; Fabre, R.; Faye, G.; Fukuhara, H.; Mathieu, A.; Sor, F. submitted to the Protein Sequence Database, March 1992 \$19481 A33754 #type complete
recombination-activating protein 1 - human
#formal name Homo sapiens #common name man
07\_sep\_1990 #sequence\_revision 07-Sep-1990 #region zinc finger motif\
#region zinc finger motif\
#region zinc finger motif\
#region zinc finger motif\
#binding site ATP (Lys) #status predicted
#length 487 #molecular-weight 55230 #checksum 1135 LISTA:RAD18 3R Chanet, R.; Magana-Schwencke, Gene (1988) 74:543-547
Potential DNA-binding domains Saccharomyces cerevisiae. Schatz, D.G.; Oettinger, M.A.; Baltimore, Cell (1989) 59:1035-1048
The V(D)J recombination activating gene, A33754 JS0082 A33754 #superfamily DNA repair protein RAD18 ATP; DNA binding; DNA repair; zinc finger JS008 Conservative 31-Dec-1993 Score 102; DB 3; Pred. No. 4.24e-04; 6; Mismatches 18; Fabre, region Ŧ : in the RAD18 N.; Fabre, F. Faye, G.; Fukuhara, H.; Length 487; on chromosome III of RAG-1. #text\_change gene ۲. product Gaps of. 1;

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KEYWORDS SUMMARY б 밁 TITLE ORGANISM RESULT S 밁 SUMMARY REFERENCE ACCESSIONS ACCESSIONS ORGANISM Matches Query Match Best Local Matches Query Match Best Local #journal #title #journal #title #cross-references MUID:90090604 #accession A33754 #cross-references Hauthors #accession #authors 293 cqicehiladpvetnckhvfcrvcilrclkvmgsycpscr 332 ##cross-references GB:M29474
DS DNA binding; zinc finger
X #length 1043 #molecular-weight 119115 #checksum ffresidues #molecule\_type mRNA #residues 1-10 Match 27.1%; Local Similarity 32.5%; ω 5 CEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTACQ 44 1 5 YKCEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTACQES 46 Similarity A43906 #type complete
nuclear phosphoprotein xnf7 - African clawed frog
#formal name Xenopus laevis #common name African clawed
31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change A43906 Tomita, H.; Soshi, T.; Inoue, H.
Mol. Gen. Genet. (1993) 238:225-233
The Neurospora uvs-2 gene encodes a protein which has homology to yeast RAD18, with unique zinc finger motifs. \$34825 #type complete
uvs2 protein Neurospora crassa
#formal name Neurospora crassa
09-Dec-1993 #sequence\_revision 09-Dec-1993 #text\_change A43906; S27947 #length 501 #molecular-weight 54830 S34825 A43906 Conservative Conservative 09-Dec-1993 MUID:92038424 1-1043 ##label SCA 1-501 ##label TOM preliminary 26.3%; Pred. Score 99; Pred. No. Score 102; DB 11; Pred. No. 4.24e-04; Mismatches Mismatches DB 12; 18; 21; Length 501; Length 1043; #checksum Indels Indels ç, 7891 6389 Gaps

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RESULT ENTRY TITLE REFERENCE ##molecule type mRNA ##reaidues 1-609 ##label RED Reddy, B.A.; Kloc, M.; Etkin, L.
Dev. Biol. (1991) 148:107-116
The cloning and characterization of a maternally expressed novel zinc finger nuclear phosphoprotein (xnf7) in Xenopu in Xenopus frog

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#gene KEYWORDS ORGANISM DATE RESULT ENTRY TITLE RESULT ENTRY TITLE ACCESSIONS REFERENCE Ś Вb GENETICS Š В SUMMARY SUMMARY KEYWORDS ORGANISM REFERENCE ACCESSIONS Query Match Best Local Matches Query Match Best Local #accession #accession #submission #authors #authors Schatz, D.G.; Oettinger, M.A.; Balt #journal Cell (1989) 59:1035-1048 #title The V(D)J recombination activating #cross-references MOJD:90090604 #accession B33754 description ##note 293 cqicehiladpvetsckhlfcricilrclkvmgsycpscr 332 141 eeltcplcvelfkdpvmvacghnfcrscidkaweggssfacpecresi 188 ##status preliminary
##molecule\_type mRNA ##cross-references GB:M29475 DS DNA binding; zinc finger W #length 1043 #molecular-weight 119490 #checksum ##residues ##molecule\_type mRNA ##cross-references NCBIN:64515; 1 DKYKCEKCHLVLCSPKQTECGHRFCESCMA-ALLSSSSPKCTACQESI 47 G 13 12 CEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTACQ h 26.0%; Similarity 32.5%; 18; Similarity Iwanejko, L.A.; Cotton, C.M.; Jones, G.W.; Tomsett, A.B.;
 Strike, P.
submitted to the EMBL Data Library, June 1995
Cloning and characterization of nuvA, an Aspergillus nidulans
 gene involved in DNA repair and recombination.
 S55494 xnf7 DNA binding; #length 609 \$55494 #type complete
C3HC4 type zinc finger protein - Emericella nidulans
#formal name Emericella nidulans, Aspergillus nidulans
O1-Aug-T995 #sequence\_revision O1-Sep-1995 #text\_change A33754 B33754 #type complete
recombination-activating protein 1 - mouse
#formal name Mus musculus #common name house mouse
07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change
31-Dec-1993 в33754 S55494 Conservative Conservative 01-Sep-1995 1-1043 ##label SCA sequence 26.3%; phosphoprotein; zinc finger
#molecular-weight 68875 #checksum :64515; NCBIP:64520; extracted from NCBI Score 98; DB 11; Pred. No. 1.61e-03; Score 99; DB 10; Pred. No. 1.16e-03; 8 6; Mismatches Mismatches M.A.; Baltimore, 19; 23; Indels EMBL:M63705 backbone Length 1043; Length 609; gene, Indels RAG-1 1; ç 6416 914 Gaps Gaps 1; 0

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SUMMARY Query Match Best Local S Matches 1 ##residues 1-477 ##label IWA ##cross-references EMBL:Z49834 #Y #noleculai / Match 25.7%; Local Similarity 34.9%; nes 15; Conservative #molecular-weight 53229 #checksum Score 97; DB 9; Pred. No. 2.24e-03, 10; Mismatches 1 Length 477; Indels 1; 6741 Gaps

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ACCESSIONS REFERENCE RESULT ENTRY TITLE SUMMARY ORGANISM #journal #title #cross-references MUID:88089405 #accession S00530 #authors ##cross-references EMBL:X06741
Y #length 328 #checksum 3305 ##molecule\_type DNA ##residues 1-3 14 Adam, R.D.; Aggarwal, A.; Lal, A.A.; de la Cruz, V.F.; McCutchan, T.; Nash, T.E.
J. Exp. Med. (1989) 167:109-118
Antigenic variation of a cysteine-rich protein in Giardia SOO530 #type fragment surface antigen CRP170 - Giardia lamblia (fragment) #formal name Giardia lamblia 31\_Dec\_1988 #sequence\_revision 31-Dec\_1988 #text\_change 18-Jun-1993 1-328 ##label ADA

1

Query Match Best Local : Matches / Match 24.9%; Local Similarity 29.4%; nes 10; Conservative Score 94; DB 9; I Pred. No. 5.99e-03; 10; Mismatches 13 13; Length 328, Indels 1; Gaps 1:

S В 211 cpaatpgc-hsscdgctenamtnqadkctgckeg 243 13 CSPKQTECGHRFCESCMAALLSSSSPKCTACQES 46

ACCESSIONS REFERENCE TITLE ORGANISM DATE RESULT #journal #title #authors 15 B42125 #type complete
cysteine-rich surface antigen 170, CRP170 - Giardia lamblia
fformal name Giardia lamblia
04-Mar-T993 #sequence\_revision 04-Mar-1993 #text\_change Adam, R.D.; Yang, Y.M.; Nash, T.E.
Mol. Cell. Biol. (1992) 12:1194-1201
The cysteine-rich protein gene family of Giardia lamblia:
loss of the CRP170 gene in an antigenic variant. 04-Mar-1993

#contents #accession #cross-references MUID:92186850 #molecule\_type #status trophozoites B42125 preliminary DNA 1-498 ##label ADA

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Page 8

SUMMARY ##cross-references NCBIN:88424; NCBIP:88431 ##note sequence extracted from NCB ##note sequence extracted from NCBI backbone
This sequence may be one segment of several.
#length 498 #molecular-weight 50111 #checksum 1456

Matches Query Match Best Local h 24.9%; Similarity 29.4%; 10; Conservative Score 94; DB 12; Pred. No. 5.99e-03; 10; Mismatches 13; Length 498 Indels 1; Gaps 1;

Ś Вb 13 CSPKQTECGHRFCESCMAALLSSSSPKCTACQES 46 96 cpaatpgc-hsscdgctenamtnqadkctgckeg 128

Search completed: Tue Job time : 25 secs. Mar 19 09:54:52 1996

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tue Mar 19 09:54:02 1996;

MasPar time 2.12 Seconds 355.211 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title:

Sequence: >US-08-404-832-3
(1-49) from US08404832.pep
1 DKYKCEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTACQESIVK

Scoring table: PAM 150 Gap 11

Searched: 43470 seqs, 15335248 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot31
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8

Statistics: Mean 31.851; Variance 57.136; scale 0.557

Pred. No. score greater than is the number of results ter than or equal to the predicted by score of the result to have a being printed,



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and is derived by analysis of the total score distribution.

#### SUMMARIES

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19.4	و ا	19.4	19.4	19.4	19.4	19.4	19.6	19.6	19.9	19.9	20.2	20.2	20.2	20.2	20.2		) N	) ( ) (	20.5	20.4	20.4	20.7	20.7	21.0	21.0	21.5	21.8	21.0	22.0	34.0	) ( ) (	22.5	л V		2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	24.9	20.0	) N		37.	27 1	27.0	20.	٥ ل د د د	46.7		Query Match
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77	PROTEIN	INDING PROTEIN			A 2		LAMININ BETA-2 CHAIN	INTEGRIN BETA-1 PRECU	PRESPORE VESICLE PROT	ICAL 13.2	LIN-IZ PROTEIN PRECUR	PROBABLE TRANSCRIPTIO				۰	HADOMARTICAL CO J AD		1. 30 8 KD	PROTEIN	ING PROTEIN	BETA-1*	INTEGRIN BETA-1 SUBUN	DP87 PROTEIN.	CYSTEINE-RICH PROTEIN	MAJOR SURFACE-LABELED	FOSTERIOR SEA COMBS F	DOWN REGULATORI PROTE	TOWNSTACTING INMISCRI	TRANSPORTING TRANSPORT		DNA BEDATE PROTEIN BA	UVBOTUETTONI 07 1 VD		CINC-BINDING PROTEIN	STANCE ANTIGEN CATT	V(U) J RECOMBINATION A	PEOPLETS.	o c	DECOMPTION OF THE	DNA BEDATE PROTETY RA	V(D).I RECOMBINATION A	-	CANCER TYPE	TNF RECEPTOR ASSOCIAT		Description
3e-	.03e-	.03e-	ωe	.03e-	.03e-	.03e-	.73e-	.73e-	.08e-	.08e-	. aye-	. dye	. 896	e dye			000	900	909	.05e~	.05e-	44e-	1.44e-01	02e-	-920		5.49e-02	3 496 03		2019510			1 100-00	0 6	2 5	2 6	1	n -		1 4	1.766-05	5.300.00	. :	06910	5 1		Pred. No.

#### ALIGNMENTS

PRT;	SE STANDARD;	ID TRF2 MOUSE AC P39429;	AB
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                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 1
                       EMBL; Z14000; HSRING1.

PIR; A47380; A47380.

HSSP; P28990; ICHC.

PROSITE; PS00518; ZINC FINGER C3HC4.

PROSITE; PS00518; ZINC FINGER PROTEIN.

ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN.

ZN FING 19 58 C3HC4-TYPE.

ZN FING 231 GLY-RICH.

DOMAIN 176 231 GLY-RICH.

DOMAIN 285 348 GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                    ZN_FING
SEQUENCE
                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; C
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                006587;
01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                           RIN1
                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SUBUNIT: HETERODIMER OF TRAF1 AND TRAF2.
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
EMBL; L35303; MMTRAF2A.
ZINC-FINGER; COLLED COIL.
ZN_FING 34 72 C3HC4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
THE RECEPTOR ASSOCIATED FACTOR 2 (TRAF2).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                    SEQUENCE FROM N.A. 93211912
LOVERING R., HANSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. 94349371
                                                                                                                                                                                                                                        RING1 PROTEIN.
      SEQUENCE
                DOMAIN
                                                                                                                                                                                                                                                                                                                                 HUMAN
                                                                                                                                                                                                                                                                                                                                                                         h 46.7%;
Similarity 45.2%;
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    501 AA;
                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                    56026 MW;
                                                                                                                                                                                                        CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
       39145 MW;
                                                                                                                                                                                                                                                                                                                                                                         Score 176; DB 7;
Pred. No. 1.71e-19;
12; Mismatches 11
GIY-RICH.
GIY-RICH.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
; 716288 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                    C3HC4-TYPE.
1264825 CN;
                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                           377
                                                                                                                                                                                                                                                                                           A.
                                                                                                                                                                                                                                                                                                                                                                          11; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Length 501;
                                                                                                                                           FREEMONT P.S.;
                                                                                                                                                                                                                                                                                                                                                                           ç,
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                           ç,
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TESULT OF THE BEST S 밁 Query Match Best Local S Matches 1 VARIANTS BC G-61, AND VARIANTS R-356; G-1038; N-1040; R-1183 & G-161
FRIEDMAN I.S., OSTERWEYER E.A., SZABO C.I., DOWD P., LYNCH E.D.,
ROWELL S.E., KING M.-C.;
NATURE GENET. 8:399-404(1994).
-!- FUNCTION: NOT KNOWN, MAY REGULATE GENE EXPRESSION.
-!- SUBCELLULAR LOCATION: NOCLEAR (POTENTIAL).
-!- DISEASE: BREAST CANCER (BC) IS AN EXTREMELY COMMON MALIGNANCY,
AFFECTING ONE IN EIGHT MOMEN DURING THEIR LIFETIME. A POSITIVE
FAMILY HISTORY HAS BEEN IDENTIFIED AS MAJOR CONTRIBUTOR TO RISK OBVELOPMENT OF THE DISEASE, AND THIS LINK IS STRIKING FOR EARLYONSET BREAST CANCER. MUTATIONS IN BRCA1 ARE THOUGHT TO BE TAVTIGIAN S., LIU Q., COCHRAN C., BENNETT L.M., DING W., BELL R., ROSENTHAL J., HUSSEY C., TRAN T., MCCLURE M., FRYE C., HATTIER T., PHELPS R., HAUGEN-STBANO A., KATCHER H., YAKUMO K., GHOLAMI Z., SHAFFER D., STONE S., BAYER S., WRAY C., BOGDEN R., DAYANANTH P., WARD J., TONIN P., NAROD S., BRISTOW P.K., NORRIS F.H., HELVERING L., MORRISON P., ROSTECK P., LAI M., BARRETT J.C., LEWIS C., NEUHAUSEN S., CANNON-ALBRIGHT L., GODLGAR D., WISEMAN R., KAMB A., SKOLNICK M.H.; CASTILIA I.H., COUCH F.J., ERDOS I GARBER J.E., BOYD J., LUBIN M.B., COLLINS F.S., WEBER B.L., NATURE GENET. 8:387-391(1994). FOTBEAL P.A., LIU Q., SHATTUCK-EIDENS D., COCHEAN C., HARSHAN K., TAVTIGIAN S., BENNETT I.M., HAUGEN-STRAND K., SWINSEN J., MIKI Y., EDDINGTON K., MCCLURE M., FRYE C., WEAVER-FELHAUS J., DING W., GHOLAMI Z., SOEDERKVIST P., TERRY L., JHANWAR S., BERCHUK A., GIGLEHART J.D., MARKS J., BALLINGER D.G., BARRETT J.C., SKOLNICK M. BRC1 KAMB A., WISEMAN R.; SCIENCE 266:120-122(1994). FUTREAL P.A., 01-FEB-1995 (REL. 01-FEB-1995 (REL. P38398; 01-0CT-1994 VARIANTS BC VARIANTS LEU-1637; 95025878 SCIENCE 266:66-71(1994). MIKI Y., SEQUENCE FROM N.A., AND VARIANT ARG-1775. EUTHERIA; PRIMATES. HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUKARYOTA; BREAST CANCER 18 HUMAN 16; Similarity SWENSEN J., GIY-64 AND GIY-1443, H.. COUCH F.J., ERDOS 31.8%; larity 34.8%; Conservative 30, CREATED)
31, LAST SEQUENCE UPDATE)
31, LAST ANNOTATION UPDATE) GLU-1708 AND ARG-1775. SHATTUCK-EIDENS D., SUSCEPTIBILITY PROTEIN. Score Pred. 11; N AND VARIANTS ALA-772 AND ASN-1040.
M.R., HOSKINS K.F., CALZONE K.,
DESHANO M.L., BRODY L.C., Mismatches 120; DB 6; No. 1.11e-08; 1863 FUTREAL P.A., Ą 18; Length 377; Indels W., BELL R.,
HATTIER T., : 3 & G-1613. E.D., Gaps ζ.

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S 뮹 SO THE THE TENT OF Matches Query Match Best Local J. CLIN. HAMEL J.C., BUYON J.P., TAN E.M.;

J. CLIN. INVEST. 87:66-76(1991).

-i- FUNCTION: ROYSSA IS A RIBONUCLEOPROTEIN PARTICLE COMPOSED OF A SINGLE POLYPEPTIDE AND ONE OF FOUR SMALL RNA MOLECULES. IT IS PRESENT IN ALL MAMMALLAN CELLS STUDIED BUT HAS NO KNOWN FUNCTION. AT LEAST TWO ISOFORMS ARE PRESENT IN NUCLEATED & RED BLOOD CELLS, AND TISSUE SPECIFIC DIFFERENCES IN ROYSSA PROTEINS HAVE BEEN IDENTIFIED. THE COMMON FEATURE OF THESE PROTEINS IS THEIR ABILLITY TO BIND HY RNAS. SSAI OR RO52.
HOMO SAPIENS (HUMAN).
HOMO SAPIENS (HUMAN). P19474; 01-FEB-1991 (REL. 17, 01-FEB-1991 (REL. 17, 01-JUN-1994 (REL. 29, VARIANT VARIANT VARIANT VARIANT VARIANT VARIANT VARIANT VARIANT ZN FING VARIANT EMBL; U14680; HS14680.
MIM; 113705; 11TH EDITION.
ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN; DISEASE MUTATION; SEQUENCE FROM N.A. 91086480 CHAN E.K., HAMEL J SEQUENCE POLYMORPHISM; 91086445 TISSUE=THYMOCYTES; SEQUENCE FROM N.A. EUTHERIA; 52 KD RO PROTEIN VARIANT VARIANT VARIANT ITOH K., 24 cpic-lelikepvstkcdhifckfcmlkllnqkkgpsqcplcknditk 70 CLIN. 5 CEKCHLVLCS-PKQTECGHRFCESCMAALLS-SSSP-KCTACQESIVK RESPONSIBLE FOR 45% OF INHERITED BREAST OF INHERITED BREAST AND OVARIAN CANCER SIMILARITY: CONTAINS A C3HC4-CLASS ZINC HUMAN 19; Similarity ITOH Y., FRANK M.B.; INVEST. 87:177-186(1991). PRIMATES 1613 1637 1708 1708 1775 1863 24 61 64 356 772 1038 1040 1183 1443 Conservative ANTI-ONCOGENE. STANDARD; A A (SJOGREN 64 61 56 356 772 1038 1040 11183 11443 11613 11613 1708 28.9%; 39.6%; 207720 LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
GREN SYNDROME TYPE A ANTIGEN CREATED) C3HC4-TYPE.

C -> G (IN BREAST CANCER).

C -> G (IN BREAST CANCER).

Q -> R.

Q -> R.

V -> A.

E -> G.

S -> N.

K -> R.

R -> G (IN BREAST CANCER).

S -> G.

S -> Score 109; Pred. No. 1. 3; VERTEBRATA; PRT; Mismatches NCER (BOC). ZINC FINGER. DB 1; L. ..06e-06; .ches 22; TETRAPODA; MAMMALIA; CANCER Length 1863; Indels (SS-A)). AND 49 MORE THAN 80% 4; Gaps

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THE SOLL THE SOLUTION TO SOLUTION CC PRIMARY SJOGERN'S SYNDROME OFTEN CONTAIN ANTIBODIES THAT REACT CC WITH NORMAL CELLULAR RO PROTEIN AS IF THIS ANTIBODIES THAT REACT CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR.

7C -- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.

8 EMBL; M34551; HSROSSA.

9 EMBL; M62800; HSSSARO.

9 PIR; A37241; A37241.

MIM; 109092; 11TH -
PROSTUME б 밁 SO FITT Query Match Best Local : Matches RIBONUCLEOPROTEIN; DNA-BINDING.

DOMAIN

24 HYDR
ZN FING
DOMAIN
25 123 B BO
DOMAIN
211 232 LEUC
DOMAIN
201 475 HYDR
CONFLICT
52 52 P ->
SEQUENCE 475 AA; 54169 MW; 11 P34088; 01-FEB-1994 (REL. 28, 01-FEB-1994 (REL. 28, 01-FEB-1994 (REL. 28, V(D)J RECOMBINATION i FUSCHIOTTI P., HARINDRANATH N., MAGE R.G., MCCORMACK W.T.,
DHANNARAJAN P., ROUX K.H.;
MOL. IMMUNDL. 30:1021-1032(1993).
-I- FUNCTION: RAG1 & RAG2 SYNERGISTICALLY ACTIVATE THE IMMUNOGLOBULIN
V-D-J RECOMBINATION. V-D-J RECOMBINATION IS THE COMBINATIONAL
PROCESS BY WHICH DEVELOPING LYMPHOCYTES BEGIN TO GENERATE THEIR
ENORMOUS RANGE OF BINDING SPECIFICITIES FROM A LIMITED AMOUNT OF
GENETIC INFORMATION. -1- SUBCELLULAR LOCATION: NUCLEAR.
-1- SIMILARIY: CONTAINS A C3HC4-CLASS ZING
EMBL, M77666; OCRACIO.
PIR; S44379; S44379.
PROSITE; PS00518; ZINC FINGER C3HC4.
ENGC-FINGER; DNA-BINDING; NUCLEAR PROTEIN.
ZN\_FING 292 330 C3HC4-TYPE. RAG1 SEQUENCE FROM N.A. 93354283 ORYCTOLAGUS CUNICULUS (RABBIT) EUKARYOTA; METAZOA; CHORDATA; SEQUENCE EUTHERIA; LAGOMORPHA. G RABIT CEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTACQESIV 12; Similarity 092; 11TH EDITION.
PS00518; ZINC FINGER C3HC4.
LUDUS ERVTHEMATOSUS; ZINC-FINGER; ANTIGEN; 292 3 1042 AA; 28.4%; larity 27.3%; Conservative STANDARD; 28,28 8, CREATED)
18, LAST SEQUENCE UPDATE)
18, LAST ANNOTATION UPDATE)
1 ACTIVATING PROTEIN. 119006 MW; Score 107; DB 6; Pred. No. 2.38e-06; 13; Mismatches 19 LEUCINE-ZIPPER.
HYDROPHOBIC.
P -> A (IN REF. C3HC4-TYPE. B BOX. HYDROPHOBIC. VERTEBRATA; PRT; -> A (IN REF. 1162917 CN; 5538604 CN; 1042 ZINC B TETRAPODA; MAMMALIA; FINGER. 2) 19; Length 475; 59 48 Indels RNA-BINDING; ç Gaps

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밁 Query Match Best Local S Matches 1 292 cqicehiladpvetsckhvfcricilrclkvmgsycpscq 331 Similarity 14; Conser Conservative 27.9%; 35.0%; Score 105; DB 6; Pred. No. 5.32e-( 7; Mismatches DB 6; .32e-06; 19; Length 1042; Indels ç, Gaps 0

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CEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTACQ

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Ş В Query Match Best Local S Matches 1 RA18 YE/ P10862; PROSITE; PS00518; ZINC FINGER C3HC4.
ZINC-FINGER; DNA-BINDING; DNA DAMAGE; DNI
ZINC-FING 28 65 C3HC4-TYPE.
ZN FING 190 210 C2HC-TYPE.
SEQUENCE 487 AA; 55230 MW; 1203687 CN JONES J.S., WEBER S., PRAKASH L.;
NUCLEIC ACIDS RES. 16.7119-7131(1988).

-!- FUNCTION: FUNCTIONS WITH DNA REPAIR PROTEIN RAD5 IN ERROR-FREE
POSTREPLICATION DNA REPAIR. RAD5 INCREASES EFFICIENCY OF RAD18 DNA REPAIR PROTEIN RAD18.

RAD18 OR YCR66W.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES. 01-JUL-1989 01-FEB-1994 EMBL; X12588; SCRAD18.
EMBL; X59720; SCCHRIII.
PIR; S05802; DDBY18.
PIR; JS0082; JS0082. CHANET R., MAGANA-SCHWENCKE GENE 74:543-547(1988). 01-ЛП-1989 88303333 SEQUENCE FROM N.A. SEQUENCE FROM N.A. BENIT -!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
-!- SUBCELLULAR LOCATION: NUCLEAR. BENIT P., CHANET R., F. YEAST 8:147-153(1992). SEQUENCE FROM N.A. ISTA; 27 rchickdflkvpvltpcghtfcslcirthlnnq-pncplc 4 FUNCTION. YEAST KCEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTAC SC00917; RAD18. Similarity 28 190 487 (REL. 11, CREATED)
(REL. 11, LAST SEQUENCE UPDATE)
(REL. 28, LAST ANNOTATION UPDATE) Conservative STANDARD; 27.1%; FABRE F., Score 102; DB 6; Pred. No. 1.76e-05; 6; Mismatches 18 z ; PRT; FAYE G., FABRE 487 Ή : DNA REPAIR; ÇŅ. FUKUHARA A 18; 65 43 Length 487; NUCLEAR PROTEIN Indels SOR F.; 1; Gaps

RESULT J

1;

RAG1\_HU P15918;

HUMAN

STANDARD;

PRT;

1043 AA

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S 밁 Query Match Best Local S Matches P33288; 01-FEB-1994 (REL. 01-FEB-1994 (REL. 01-FEB-1994 (REL. HSSP; P28990; 1CHC.

MIM; 179615; 11TH EDITION.

PROSITE; PS00518; ZINC FINGER C3HC4.

ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN.

211C-TYPE. UVS2 HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES. 01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-MOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
V(D)J RECOMBINATION ACTIVATING PROTEIN. TOMITA H., SOSHI T., INOUE H.;
MOL. GEN. GENET. 238:225-233(1993).
-!- FUNCTION: MAY BE AN ACTIVATOR THAT FUNCTIONS
OF DNA REPAIR GENES.
-!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE). GENETIC INFORMATION.

-i- SUBCELLULAR LOCATION: NUCLEAR.

-i- TISSUE SPECIFICITY: MATURING LYMPHOID CELLS.

-i- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER. -!- FUNCTION: RAGI & RÁGZ SYNERGISTICALLY ACTIVATE THE IMMUNOGLOBULIN V-D-J RECOMBINATION IS THE COMBINATORIAL PROCESS BY WHICH DEVELOPING LYMPHOCYTES BEGIN TO GENERATE THEIR ENORMOUS RANGE OF BINDING SPECIFICITIES FROM A LIMITED AMOUNT OF STRAIN=C1-T10-34A; SEQUENCE FROM N.A. NEUROSPORA CRASSA. EUKARYOTA; FUNGI; UVS-2 EMBL; M29474; HSRAG1. PIR; A33754; A33754. SCHATZ SEQUENCE FROM N.A. 293 cqicehiladpvetnckhvfcrvcilrclkvmgsycpscr 332 ß TZ D.G., OETTINGER M.A., 59:1035-1048(1989). NEUCR PROTEIN h 27.1%; Similarity 32.5%; 13; Conservative 1043 AA; STANDARD; 28,28 ASCOMYCOTINA; PYRENOMYCETES; SORDARIALES 331 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE) 119115 MW; Score 102; DB 6; Pred. No. 1.76e-05; 9; Mismatches 18 BALTIMORE C3HC4-TYPE. SW; 5512008 CN; 501 . :: Ą 18; Length 1043; N Indels THE TRANSCRIPTION 0 Gaps

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290 cqicehiladpvetsckhlfcricilrclkvmgsycpscr 329

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                                                                                       SQ FTT SQ DR
                                            Query Match
Best Local S
Matches 1
                                                                                    EMBL; D11458; NCIVS2.
PIR; S24825; S34825.
PROSITE; PS00518; ZINC FINGER C3HC4.
ZINC-FINGER; DNA-BINDING; DNA-DAMAGE; DNF
ZN FING 34 71 C3HC4-TYPE.
ZN FING 189 209 C2HC-TYPE.
ZN-FING 189 209 C2HC-TYPE.
                                                                                                                                                                !- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER
Similarity 36.4%; 16; Conservative
                                                      26.3%;
                                         Score 99; DB 7; I
Pred. No. 5.76e-05;
6; Mismatches 21
                                                                                                                      DNA
                                                                                       ÇN;
                                                                                                                      REPAIR;
                                            21;
                                                                Length 501;
                                                                                                                        NUCLEAR PROTEIN.
                                             Indels
                                             ۲.
                                             Gaps
                                             ۲.
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Query Match
Best Local S
Matches 1
                                                                                                           GENETIC INFORMATION.

-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFICITY: MATURING LYMPHOID CELLS.
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
EMBL; M29475; MMTAGIA.
PIR; B33754; B33754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAG1 MOUSE STANDARD; PRT; 1040 AA. p15913; 01-APR-1990 (REL. 14, CREATED) 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE) 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE) V(D)J RECOMBINATION ACTIVATING PROTEIN.
                                                                                                                                                                                             SADOFSKY M.J., HESSE J.E., MCBLANE J.F., GELLERT M.;
NUCLEIC ACIDS RES. 21:5644-5650(1993).
-!- FUNCTION: RAG1 & RAG2 SYNERGISTICALLY ACTIVATE THE IMMUNOGLOBULIN
-!- FUNCTION: RAG1 WHICH DEVELOPING LYMPHOCYTES BEGIN TO GENERATE THEIR
PROCESS BY WHICH DEVELOPING LYMPHOCYTES BEGIN TO GENERATE THEIR
ENORMOUS RANGE OF BINDING SPECIFICITIES FROM A LIMITED AMOUNT OF
                                                                                                                                                                                                                                                                                                                                                                                              MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; C
EUTHERIA; RODENTIA.
                                                        SEQUENCE
                                                                    ZINC-FINGER;
ZN FING
                                                                                                                                                                                                                                                                                                                           SCHATZ D.G., OETTINGER M.A., CELL 59:1035-1048(1989).
                                                                                                                                                                                                                                                                                                                                                      90090604
                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Similarity 13; Conser
                                                                   PSÖ0518; ZINC FINGER C3HC4.
GER; DNA-BINDING; NUCLEAR PROTEIN.
290 328 C3HC4-TYPE.
                                                       290
1040 AA;
 26.0%;
llarity 32.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              CHORDATA;
                                                          119160 MW;
 Score 98; DB 6;
Pred. No. 8.52e-05
8; Mismatches 1
                                                        C3HC4-TYPE.
MW; 5499298 CN;
                                                                                                                                                                                                                                                                                                                                           BALTIMORE D.;
                                                                                                                                                                                                                                                                                                                                                                                                               VERTEBRATA; TETRAPODA; MAMMALIA;
  Mismatches 19;
                              Length 1040;
  Indels
  ç
  Gaps
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CEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTACQ 44

UL-APR-1990 (REL. 14, CREATED)

Ol-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)

Ol-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)

SURFACE ANTIGEN CRP170 (FRAGMENT).

GIARDIA LAMBLIA.

C170 GIALA P15799; 01-APR-1990 01-APR-1990 01-APR-1990

STANDARD;

328

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LT 11
A33 PLEWA STANDARD; PRT; 624 AA.
Q02089;
01-QCT-1994 (REL. 30, CREATED)
01-QCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-QCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
2INC-BINDING PROTEIN A33.
PLEURODELES WALTLII (IBERIAN RIBBED NEWT)
PLEURODELES WALTLII (IBERIAN RIBBED NEWT)
                                                                                                           BELLINI M., LACROIX J.-C., GALL J.G.;

EMBO J. 12:107-114 (1993).

-!- FUNCTION: MAY BE A NUCLEAR REGULATORY PROTEIN THAT IS STORED
IN THE GERMINAL VESICLE FOR USE DURING EARLY EMBRYOGENESIS
AND MAY PLAY A ROLE IN THE SYNTHESIS OR PROCESSING OF PRE-MRNA
DURING OOGENESIS.
                                                                                                                                                                                                           93154311
                                                                                                                                                                                                                         TISSUE=OVARY;
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      CAUDATA.
                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                (IBERIAN RIBBED NEWT).
CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA;
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S 밁 STITITION COCCOCC Query Match Best Local Matches ZN FING DOMAIN DOMAIN DOMAIN SEQUENCE DOMAIN HEPTAD DOMAIN -!- DEVELOPMENTAL STAGE: IT FIRST APPEARS ON THE CHROMOSOME LOOPS AND IN THE NUCLEOPLASM OF THE GERMINAL VESICLE (GV). IT IS TRANSMITTED TO THE EGG AT GV BREAKDOWN AND APPEARS IN EMBYBONIC NUCLEI AT THE MID-BLASTULA STAGE AND IS FOUND IN MANY BUT NOT ALL NUCLEI AT STILL LATER STAGES OF EMBRYOGENESIS.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SUBCELLULAR LOCATION: A C3HC4-CLASS ZINC FINGER. EMBL; L04190; PWPWA33A. ZINC-FINGER; NUCLEAR PR 158 edltcplcrslfkepvilecghnfckhcidkswesasafscpecke 1 DKYKCEKCHLVLCSPKQTECGHRFCESCMAALLSSSSP-KCTACQE REPEAT PATTERN; RNA-BINDING Similarity 15; Conse 624 AA; NUCLEAR PROTEIN; DEVELOPMENTAL PROTEIN; Conservative 149 201 269 386 619 24.9%; 71056 MW; Score 94; DB 1; Pred. No. 4.01e-04 7; Mismatches 2 COILED COIL. RFP-LIKE. в вох. C3HC4-TYPE. NUCLEAR LOCALIZATION NUCLEAR LOCALIZATION 2025970 CN; 23; Length 624; SIGNAL Indels 45 COILED COIL; (POTENTIAL). ۲. Gaps 1;

RESULT RESULT AND RESULT RESUL

88089405

SEQUENCE FROM N.A. STRAIN=ISOLATE WB;

HEXAMITIDAE.

PROTOZOA; SARCOMASTIGOPHORA; MASTIGOPHORA; DIPLOMONADIDA;

ADAM R.D., AGGARWAL A., NASH T.E.;

LAL A.A.,

DΕ

F

CRUZ V.F.,

MCCUTCHAN

. EXP. MED. 167:109-118(1988)

RESULT
ACC PRINCE POR PRINCE P CARLSON L.M., OETTINGER M.A., SCHATZ D.G., MASTELLER E.L.,
HURLEY E.A., MCCORMACK W.I., BALTIMORE D., THOMPSON C.B.,
CELL 64:201-208(1991),
-i- FUNCTION: RAG1 6 RAG2 SYNERGISTICALLY ACTIVATE THE IMMUNOGLOBULIN
V-D-J RECOMBINATION. V-D-J RECOMBINATION IS THE COMBINATORIAL
PROCESS BY WHICH DEVELOPING LYMPHOCYTES BEGIN TO GENERATE THEIR
ENORMOUS RANGE OF BINDING SPECIFICITIES FROM A LIMITED AMOUNT OF
GENETIC INFORMATION. 01-MAR-1992 (REL. 21, CREATED)
01-MAR-1992 (REL. 21, IAST SEQUENCE UPDATE)
01-MAR-1992 (REL. 21, IAST ANNOTATION UPDAT
V(D)J RECOMBINATION ACTIVATING PROTEIN. RAG1 CHI P24271; EMBL; M58530; PIR; S42509; SEQUENCE PROSITE; PS00518; ZINC-FINGER; DNA-ZN FING -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SIMILARITY: CONTAINS A C3HC4-CLASS GALLIFORMES. EUKARYOTA; METAZOA; GALLUS GALLUS SEQUENCE FROM N.A. CHICK 284 3 1041 AA; 00518; ZINC FINGER C3HC4.

DNA-BINDING; NUCTEAR PROTEIN.
284 327 C3HC4-mvmm GGRAG1G. (CHICKEN) STANDARD; CHORDATA; 119916 MW; C3HC4-TYPE. W; 5442207 CN; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE; PRT; 1041 AA ZINC FINGER.

Б В

211 cpaatpgc-hsscdgctenamtngadkctgckeg 243

13 CSPKQTECGHRFCESCMAALLSSSSPKCTACQES 46

Matches

10;

Conservative

Query Match Best Local Similarity

24.9%;

Score 94; Pred. No. 10; Misma

DB 1; 1

Length 328; Indels

Mismatches

13;

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NON TER SEQUENCE

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REPEAT; NON TER REPEAT

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4MT2.

-!- CYSTEINE-RICH, ANTIGENICALLY VARIANT SURFACE PROTEIN EMBL; X06741; GLCRP170.
PIR; S00530; S00530.

Query Match Best Local Similarity

24.9%; 30.8%;

Score 94; DB 6; I Pred. No. 4.01e-04;

Length

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Page 8

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RESULT
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AC P.
DT 0
DT 0
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GN R HE SOLT HE SOL S 밁 S 밁 Query Match Best Local : Matches Matches 01-FEB-1994 01-FEB-1994 01-JUN-1994 PIR; S28290; SZ6250.

PIR; S28290; SZ6250.

PROSTITE; PS0518; ZINC FINGER C3HC4.

PROSTITE; PS0518; ZINC FINGER; DNA-BINDING; NUCLEAR PROTEIN.

HYPOTHETICAL PROTEIN; ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN.

R 45

7N FING

7N FING

18675 MW; 132007 CN; YNN1 CAEEL Q03605; Q1-FEB-1994 Q1-FEB-1994 Q1-JUN-1994 WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON I
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
LATREILLE P., LICHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., NATURE 368:32-38(1994).
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
EMBL; Z19156; CET02C1.
PIR; S28290; S28290. HYPOTHETICAL R05D3.4. YNC4 P34537; WOHLDMAN STRAIN=BRISTOL N2; SEQUENCE FROM N.A. CAENORHABDITIS ELEGANS EUKARYOTA; METAZOA; ACC HYPOTHETICAL 289 G 13 1\_CAEEL edfccavcldffvepciiecghsycrfcieshlnine~kcplcr 46 : | | | | | | | : | : | | | |: CEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTAC cqicehiladpvettcrhlfcrtcilscirvmgcycpsc 327 DKYKCEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTACQ CAEEL Similarity 12; 1 (REL. 28, CREATED) 1 (REL. 28, LAST SEQU 1 (REL. 29, LAST ANNO 1 18.7 KD PROTEIN TO (REL. (REL. (REL. 97.1 23.9%; larity 29.5%; Conservative Conservative STANDARD; STANDARD; 在 29 28 1 ACOELEMATES; NEMATODA; SECERNENTEA; RHABDITIDA. CREATED)
, LAST SEQUENCE UPDATE)
, LAST ANNOTATION UPDATE)
, LAST ANNOTATION UPDATE)
PROTEIN ROSD3.4 IN CHROMOSOME III. LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
PROTEIN TO2C1.1 IN CHROMOSOME III. Score 90; DB 8; I Pred. No. 1.84e-03; 9; Mismatches 21 9; PRT; Mismatches 834 160 B æ 43 21; 18; Length 160; Indels 44 Indels SHOWNKEEN R., 1: ç Gaps Gaps

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Listing for Mary Hale

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Best Local Similarity
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01-OCT-1993
01-FEB-1994
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
FULTON L., GARDNER A., GREEN P., HEMKINS T., HILLER L., JIER M.,
JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
LATREILLE P., LICHTNING J., LLOYD C., MORTIMORE B., O'CALLACHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SOUNHAMMER E., STADEN R.,
SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WORMPEP; ROSD3.4; CE00283.

PROSITE; PS00518; ZINC FINGER C3HC4.

HYPOTHETICAL PROTEIN; ZINC-FINGER; DNA-BINDING;

ZN FING 782 820 C3HC4-TYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA REPAIR PROTEIN RAD5.

RAD5 OR REV2 OR SNN2.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NATURE 368:32-38(1994).
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAENORHABDITIS ELEGANS
EUKARYOTA; METAZOA; ACI
AHNE F., BAUR M., ECKARDT-SCHUPP F.;
CURR. GENET. 22:277-282(1992).
-i- FUNCTION: PROBABLE HELICLASE, FUNCTIONS WITH DNA REPAIR PROTEIN
RAD18 IN ERROR-FREE POSTREPLICATION DNA REPAIR. INVOLVED IN TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P32849;
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                                                                                                                                                                 SEQUENCE OF 402-1063 FROM N.A. 93008350
                                                                                                                                                                                                                                                                                         MOL. CELL.
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PRAKASH L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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YEAST
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S44866; S44866.
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834 AA;
                                                                                                                                                                                                                                                                                             BIOL.
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(REL. 27, LAST SEQUENCE UPDATE)
(REL. 28, LAST ANNOTATION UPDATE)
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larity 32.1%;
Conservative
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Pred. No. 1.18e-02;
7; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                         PETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                     T.D.,
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                                                                                                                                                                                                                                                                                                                                                                         BANKMANN M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHABDITIDA.
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PROSITE; PS00518; ZINC FINGER C3HC4.

PROSITE; PS00518; ZINC FINGER C3HC4.

PROSITE; PS00518; ZINC FINGER; ZINC-FINGER; DNA-BINDING;

WAS DAMAGE; DNA REPAIR; NUCLEĀR PROTEIN; ZINC-FINGER; DNA-BINDING;

WAS HELICASE; ATP-BINDING.

ASP/GLU-RICH (ACIDIC).

TOMAIN

303

315

ARG/LYS-RICH (BASIC).

TOMAIN

303

315

ATP (POTENTIAL).

TOMAIN

520

TOMAIN

532

539

ATP (POTENTIAL).

TOMAIN

532

539

ATP (POTENTIAL).

TOMAIN

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578

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Best Local Similarity 75.0%;
Matches 9; Conservative
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-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
-!- SIMILARITY: TO HELICASES OF THE SNF2/RAD54 FAMILY.
EMBL; M96644; SCRAD5A.
EMBL; 43248; S43248.
EMBL; 43248; S43248.
EMBL; 5431301; S431301.
PIR; S25983; S26983.
PIR; S26983; S26983.
ELISTA; SC00924; RAD5.
                                                                                                                                          930 tecghsfcekcl 941
||||| ||| |:
18 TECGHRFCESCM 29
                                                                                                                                                                                                                                                                                             Score 85; DB 6; Ler
Pred. No. 1.18e-02;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                      Length 1169;
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